

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 00:41:05 ; Search time 8878.33 Seconds  
(without alignments)  
12582.818 Million cell updates/sec

Title: US-09-830-972-1  
Perfect score: 3741  
Sequence: 1 attgctcgtctctgggcggcg.....gattgaagcgcaaagcagat 3741

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Query						Description
	No.	Score	Match	Length	DB	ID	
	1	772.4	20.6	969	13	BU839934	BU839934 AGENCOURT
	2	767.2	20.5	785	14	CA511870	CA511870 UI-R-FJ0-
	3	753.4	20.1	842	13	BU709149	BU709149 UI-M-EW0-
	4	745	19.9	896	14	CB204418	CB204418 AGENCOURT
c	5	725.6	19.4	796	14	CA504729	CA504729 UI-R-FJ0-
	6	709.8	19.0	805	12	BI730192	BI730192 603349739
	7	709.4	19.0	822	14	CB521332	CB521332 UI-M-GH0-
	8	707.8	18.9	986	13	BU841009	BU841009 AGENCOURT
	9	678.4	18.1	772	14	CF948588	CF948588 UI-M-HJ0-
	10	673.6	18.0	778	13	BU709106	BU709106 UI-M-EW0-
	11	662.6	17.7	777	14	CA320618	CA320618 UI-M-FW0-
	12	660.4	17.7	802	14	CA320635	CA320635 UI-M-FW0-
	13	659.2	17.6	951	13	BQ892001	BQ892001 AGENCOURT
	14	651.2	17.4	767	14	CF726835	CF726835 UI-M-HB0-
	15	648.6	17.3	739	13	BU612951	BU612951 UI-M-FR0-
	16	644.4	17.2	726	14	CF737320	CF737320 UI-M-HD0-
	17	638.4	17.1	724	14	CF729503	CF729503 UI-M-HD0-
	18	638.4	17.1	742	14	CA320833	CA320833 UI-M-FW0-
	19	638	17.1	638	14	CB576696	CB576696 AMGNNUC:C
	20	633.8	16.9	779	14	CB244702	CB244702 UI-M-FY0-
	21	633.4	16.9	862	9	AU079375	AU079375 AU079375
	22	617.6	16.5	688	14	CF540092	CF540092 UI-M-EX0-
	23	616	16.5	700	12	BI664179	BI664179 603289106
	24	608.2	16.3	935	13	BQ963057	BQ963057 AGENCOURT
	25	606.8	16.2	751	14	CA315995	CA315995 UI-M-FW0-
	26	605	16.2	673	14	CD349457	CD349457 UI-M-FY0-
	27	604.8	16.2	623	14	CB578453	CB578453 AMGNNUC:C
	28	604.8	16.2	691	13	BU707644	BU707644 UI-M-FR0-
	29	602	16.1	913	14	CB845105	CB845105 M2PN-0675
	30	598	16.0	609	14	CB580803	CB580803 AMGNNUC:N
	31	589.2	15.7	914	9	AU079162	AU079162 AU079162
	32	574.2	15.3	782	12	BI739239	BI739239 603359521
	33	570	15.2	810	12	BG668013	BG668013 DRABTB12
	34	568.6	15.2	698	13	BU058441	BU058441 UI-M-FO0-
	35	561	15.0	624	14	CB578355	CB578355 AMGNNUC:N
	36	561	15.0	646	9	AA791734	AA791734 vu08b07.r
	37	561	15.0	964	13	BQ900768	BQ900768 AGENCOURT
	38	560	15.0	681	14	CF742144	CF742144 UI-M-HB0-
	39	560	15.0	3533	11	AK034902	AK034902 Mus muscu
c	40	559.8	15.0	567	12	BI289826	BI289826 UI-R-DK0-
	41	556.8	14.9	717	13	BY756291	BY756291 BY756291
	42	556	14.9	556	14	CB613337	CB613337 AMGNNUC:N
	43	550.8	14.7	588	10	BF563033	BF563033 UI-R-B01-
	44	547.4	14.6	691	14	CB525239	CB525239 UI-M-FY0-
	45	546.8	14.6	817	14	CA322433	CA322433 UI-M-FX0-

## ALIGNMENTS

RESULT 1  
 BU839934  
 LOCUS BU839934 969 bp mRNA linear EST 16-OCT-2002  
 DEFINITION AGENCOURT\_8947611 NIH\_MGC\_130 Mus musculus cDNA clone IMAGE:6329890  
 5', mRNA sequence.  
 ACCESSION BU839934  
 VERSION BU839934.1 GI:24024317  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 969)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,  
 Ph.D.  
 cDNA Library Preparation: ResGen, Invitrogen Corp  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM13783 row: g column: 11  
 High quality sequence stop: 651.  
 FEATURES Location/Qualifiers  
 source 1. .969  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:6329890"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_130"  
 /note="Organ: otocysts; Vector: pCMV-SPORT6.1; Site\_1:  
 EcoRV; Site\_2: NotI; Cloned unidirectionally. Primer:  
 Oligo dT. Average insert size 1.95 kb. Constructed by  
 ResGen, Invitrogen Corp. Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 20.6%; Score 772.4; DB 13; Length 969;  
 Best Local Similarity 89.6%; Pred. No. 1.3e-103;  
 Matches 878; Conservative 0; Mismatches 88; Indels 14; Gaps 4;

Qy 2172 CATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAGCCTGAAAGTTT 2231  
 ||||| ||||||||||||| | | || ||||||||| ||| |||||||||||||||||  
 Db 1 CATGAGTGTAGCACTAAAACATCGGACTCAAAGGAAGAAATTAAAGAGCCTGAAAGTTT 60  
 ||||| ||||||||||||| ||||||| ||||||||||||||||||||| |||||||||  
 Qy 2232 TAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGTGATTTAATTAA 2291  
 ||||||||| ||||||| ||||||||||||||||||||| ||||||||| |||||||||

Db 61 TAATGCAGCTGCTCAGGAAGCAGAAGCTCCTTATATATCCATTGCATGTGATTTAATTAA 120  
 Qy 2292 AGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTCTCTAATTATTTCAGAAATAGCAAA 2351  
 |||||  
 Db 121 AGAAACAAAGCTCTCCACTGAGCCAAGTCCAGAGTTCTCTAATTATTTCAGAAATAGCAAA 180  
 Qy 2352 ATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGAGGATTCTCTCACCTGAATCTGA 2411  
 ||| ||||| || ||| ||||| ||||| ||||| |||||  
 Db 181 ATTTGAGAAGTCGGTGCCCTGATCACTGTGAGCTCGTGATGATTCTCTACCCGAATCTGA 240  
 Qy 2412 ACCAGTTGACTTATTTAGTGATGATTTCGATTCTCTGAAGTCCCACAAACACAAGAGGAGGC 2471  
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 Db 241 ACCAGTTGACTTATTTAGTGATGATTCAATTCTCTGAAGTCCCACAAACACAAGAGGAGGC 300  
 Qy 2472 TGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCCCAGCACAAA-- 2529  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 301 TGTGATGCTAATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAACACAACACAAACA 360  
 Qy 2530 -GAGGAGAGACTTAGTGCCCTCACCTCAGGAGCTAGGAAAGCCATATTTAGAGTCTTTTCA 2588  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 361 TAAGGAGAGACTTAGTGCTTCACCTCAGGAGGTAGGAAAGCCATATTTAGAGTCTTTTCA 420  
 Qy 2589 GCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTGACCAAAAA 2648  
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 Db 421 GCCCAATTTACATATTACAAAAGATGCTGCATCTAATGAAATTCCAACATTGACCAAAAA 480  
 Qy 2649 GGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAATGATGACTT 2708  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 481 GGAGACAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCCAATGATGACTT 540  
 Qy 2709 ACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCATCTCCGAT 2768  
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 Db 541 ACTTTCTTCTAAGGAAGACAAAATGAAAGAAAGTGAAACATTTTCAGATTCATCTCCCAT 600  
 Qy 2769 TGAGATAATAGATGAATTTCCACGTTTGTGAGTGCTAAAGATGATTCTCCTAAATTAGC 2828  
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 Db 601 TGAGATAATAGATGAGTTTCCACATTTGTGAGTGCTANAGATGATTCTCCT----- 652  
 Qy 2829 CAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATCCAAAGCGG 2888  
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 Db 653 -AAGGAGTACACTGACCTAGAAGTATCCAACAAAAGTGAAATTGCTAATGTCCAGAGCGG 711  
 Qy 2889 GGCAGATTCAATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAATATATATCC 2948  
 || ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 712 NGCCAATTCGTTGCCTTGCTCAGAATTGCCCTGTGACCTTTCTTTCAAGAATACATATCC 771  
 Qy 2949 TAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGC 3008  
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 Db 772 TAAAGATGAAGCACATGTCTCAGATGAATTCT-CAAAAGTAGGTCCAGTGTATCTAAGGT 830  
 Qy 3009 ATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGT 3068  
 || ||| || ||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 831 GCCCCTATTGCTTCCCAATGGTTTCTGCTTGGAATCTCAAATAG-AATGGGCCACATAGT 889  
 Qy 3069 TAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGA 3128  
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 Db 890 TTAACCCCAAAGTACTTACGGAAGAAGCAGAGGAAAAAACTTCCTTCTTGATCCGAGAAAGA 949



Qy 3129 GGACAGATCCCTGTCAGCTG 3148  
 || ||||| |||||  
 Db 950 GGGACGATCCCTGACAGCTG 969

RESULT 2  
 CA511870

LOCUS CA511870 785 bp mRNA linear EST 15-NOV-2002  
 DEFINITION UI-R-FJ0-cpx-e-15-0-UI.r1 UI-R-FJ0 Rattus norvegicus cDNA clone  
 UI-R-FJ0-cpx-e-15-0-UI 5', mRNA sequence.

ACCESSION CA511870

VERSION CA511870.1 GI:25002824

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE 1 (bases 1 to 785)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene  
 discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: Soares, MB

Coordinated Laboratory for Computational Genomics  
 University of Iowa

375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. James Lin, Universtiy of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com).

Seq primer: M13 REVERSE.

FEATURES

source

Location/Qualifiers

1. .785

/organism="Rattus norvegicus"

/mol\_type="mRNA"

/strain="Sprague-Dawley"

/db\_xref="taxon:10116"

/clone="UI-R-FJ0-cpx-e-15-0-UI"

/tissue\_type="embryo"

/dev\_stage="embryo"

/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone\_lib="UI-R-FJ0"

/note="Vector: pYX-Asc; Site\_1: EcoR I; Site\_2: Not I;

UI-R-FJ0 is a cDNA library containing the following

tissue(s): rat embryo. The library was constructed

according to Bonaldo, Lennon and Soares, Genome Research,

6:791-806, 1996. First strand cDNA synthesis was primed

with an oligo-dT primer containing a Not I site. Double

stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CATCTCTACT. This library was created for the University of Iowa Program for Rat Gene Discovery and Mapping (Val Sheffield, Bento Soares and Tom Casavant)"

# ORIGIN

```

Query Match          20.5%;  Score 767.2;  DB 14;  Length 785;
Best Local Similarity 99.2%;  Pred. No. 7.7e-103;
Matches 780;  Conservative 0;  Mismatches 5;  Indels 1;  Gaps 1;

Qy      1699  ATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTCCTTG TAGCAGTACAGGATTCT 1758
          |||
Db        1  ATAACAGAGAAGACTATCCCCACAACGTCAAATCCTTTCCTTG TAGCAGTACAGGATTCT 60

Qy      1759  GAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACTGAGGCAGCAGTGTCAAAC 1818
          |||
Db        61  GAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACTGAGGCAGCAGTGTCAAAC 120

Qy      1819  ATGCCTGAAGGTCTGACGCCAGATTTAGTTTCAGGAAGCATGTGAAAGTGAAGTGAATGAA 1878
          |||
Db       121  ATGCCTGAAGGTCTGACGCCAGATTTAGTTTCAGGAAGCATGTGAAAGTGAAGTGAATGAA 180

Qy      1879  GCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTGGTCCAAACATCAGAAGCT 1938
          |||
Db       181  GCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTGGTCCAAACATCAGAAGCT 240

Qy      1939  ATACAAGAATCACTTTACCCACAGCACAGCTTTGCCCATCATTTGAGGAAGCTGAAGCA 1998
          |||
Db       241  ATACAAGAATCACTTTACCCACAGCACAGCTTTGCCCATCATTTGAGGAAGCTGAAGCA 300

Qy      1999  ACTCCGTCACCAGTTTTGCCTGATATTGTTATGGAAGCACCATTAAATTCTCTCCTTCCA 2058
          |||
Db       301  ACTCCGTCACCAGTTTTGCCTGATATTGTTATGGAAGCACCATTAAATTCTCTCCTTCCA 360

Qy      2059  AGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCACTGGAAGCACCTCCTCCAGTT 2118
          |||
Db       361  AGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCACTGGAAGCACCTCCTCCAGTT 420

Qy      2119  AGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCACCATATGAAGAAGCCATGAAT 2178
          |||
Db       421  AGTTATGACAGTATAAAGCTTGAGCCTGAAAATCCCCACCATATGAAGAAGCCATGAAT 480

Qy      2179  GTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAGCCTGAAAGTTTTAATGCA 2238
          |||
Db       481  GTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAGCCTGAAAGTTTTAATGCA 540

Qy      2239  GCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGTGATTTAATTAAAGAAACA 2298
          |||
Db       541  GCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGTGATTTAATTAAAGAAACA 600

Qy      2299  AAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTCAGAAATAGCAAAATTCGAG 2358
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Db          601 AAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTTCAGAAATAGCANAATTCGAG 660
Qy          2359 AAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCCTCACCTGAATCTGAACCAGTT 2418
            |||
Db          661 AAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCCTCACCTGAATCTGAACCAGTT 720
Qy          2419 GACTTATTTAGTGATGATTCGATTCCTGAAGTCCCACAAACACAAGAGGAGGCTGTGATG 2478
            |||
Db          721 GACTTATTTAGTGATGATTCGATTCCTGAAGT-CCACANACACAAGAGGAGGCTGTGATG 779
Qy          2479 CTCATG 2484
            |||
Db          780 CTCATG 785

```

# RESULT 3

BU709149

LOCUS BU709149 842 bp mRNA linear EST 15-JUL-2003

DEFINITION UI-M-EW0-caz-o-10-0-UI.r1 NIH\_BMAP\_EW0 Mus musculus cDNA clone  
IMAGE:6419553 5', mRNA sequence.

ACCESSION BU709149

VERSION BU709149.1 GI:23642332

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 842)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Dr. James Lin, Univeristy of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)

Seq primer: pYX-5.

## FEATURES

source

Location/Qualifiers

1. .842

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6"

/db\_xref="taxon:10090"

/clone="IMAGE:6419553"

/tissue\_type="whole brain"

/dev\_stage="embryo 15.5 dpc"

/lab\_host="DH10B (T1 phage resistant)"

/clone\_lib="NIH\_BMAP\_EW0"

/note="Organ: brain; Vector: pYX-Asc; Site\_1: EcoR I;

Site\_2: Not I; The library was constructed according to

Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is GTGCGTGGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

# ORIGIN

```

Query Match          20.1%;  Score 753.4;  DB 13;  Length 842;
Best Local Similarity 94.2%;  Pred. No. 8.2e-101;
Matches 792;  Conservative 0;  Mismatches 48;  Indels 1;  Gaps 1;

Qy      1677 AGAAGAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTT 1736
        |||
Db      2    AGAAGAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTT 61

Qy      1737 CCTTGTTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGT 1796
        |||
Db      62    CCTTGTTAGCAATACATGATTCTGAGGCAGATTATGTCACAACAGATAATTTATCAAAGGT 121

Qy      1797 GACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGC 1856
        |||
Db      122   GACTGAGGCAGTAGTGGCAACCATGCCTGAAGGTCTAACGCCAGATTTAGTTCAGGAAGC 181

Qy      1857 ATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGGA 1916
        |||
Db      182   ATGTGAAAGTGAAGTGAACGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGGA 241

Qy      1917 CTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTGCCC 1976
        |||
Db      242   CTTGGTCCAGACATCAGAAGCTATACAAGAGTCAATTTACCCACAGCACAGCTTTGCCC 301

Qy      1977 ATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATGGAAGC 2036
        |||
Db      302   ATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATGGAAGC 361

Qy      2037 ACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCC 2096
        |||
Db      362   GCCATTAAATTCTCTCCTTCCAAGCACTGGTGCTTCTGTAGCGCAGCCCAGTGCATCCCC 421

Qy      2097 ACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCC 2156
        |||
Db      422   ACTAGAAGTACCGTCTCCAGTTAGTTATGACGGTATAAAGCTTGAGCCTGAAAATCCCCC 481

Qy      2157 ACCATATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAA 2216
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Db      482   ACCATATGAAGAAGCCATGAGTGTAGCACTAAAACATCGGACTCAAAGGAAGAAATTAA 541

Qy      2217 AGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGC 2276
        |||
Db      542   AGAGCCTGAAAGTTTTAATGCAGCTGCTCAGGAAGCAGAAGCTCCTTATATATCCATTGC 601

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Qy 2277 GTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTA 2336  
 |||  
 Db 602 ATGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGAGTTCTCTAATTA 661  
 Qy 2337 TTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTC 2396  
 |||  
 Db 662 TTCAGAAATAGCANAATTTGAGAAGTCGGTGCCTGATCACTGTGAGCTCGTGGATGATTC 721  
 Qy 2397 CTCACCTGAATCTGAACCAAGTTGACTTATTTAGTGATGATTCGATTCCTGAAGTCCCACA 2456  
 |||  
 Db 722 CTCACCCGAATCTGAACCAAGTTGACTTATTTAGTGATGATTCGAATTCCTGAAGT-CCACA 780  
 Qy 2457 AACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGT 2516  
 |||  
 Db 781 NACACAAGAGGAGGCTGTGATGCTAATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGT 840  
 Qy 2517 A 2517  
 |  
 Db 841 A 841

#### RESULT 4

CB204418

LOCUS CB204418 896 bp mRNA linear EST 05-FEB-2003

DEFINITION AGENCOURT\_11276017 NIH\_MGC\_135 Mus musculus cDNA clone  
 IMAGE:30138586 5', mRNA sequence.

ACCESSION CB204418

VERSION CB204418.1 GI:28241848

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 896)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Dr. David Rowe

cDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDAM0041 row: k column: 11

High quality sequence stop: 686.

#### FEATURES

source

Location/Qualifiers

1. .896

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="IMAGE:30138586"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_135"

/note="Vector: pCMVSPORT6.1; Site\_1: EcoRV; Site\_2: NotI; Normalized full-length enriched library from pooled mouse embryonic limb, maxilla and mandible, day 12.5, 13.5, 14.5, and 15.5 (size selected for the 0.5-1 kb fragments) Cloned directionally, priming method: Oligo-dT. cDNA enrichment: >1k bp, Average insert size 1.6k bp. Normalization (Cot value): 7.5 kb. Priming sequence: 5'GACTAGTTCTAGATCGCGAGCGGCCGCC(T)3' Tissue contributed by, David Rowe. Library constructed by ResGen, Invitrogen Corp."

# ORIGIN

Query Match 19.9%; Score 745; DB 14; Length 896;  
 Best Local Similarity 93.0%; Pred. No. 1.4e-99;  
 Matches 816; Conservative 0; Mismatches 50; Indels 11; Gaps 3;

Qy	2745	AACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTCAGTGC	2804
Db	13	AACATTTTCGATTTCATCTCCCATTCGAGATAATAGATGAGTTTCCACATTTGTCAGTGC	72
Qy	2805	TAAAGATGATTCTCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAG	2864
Db	73	TAAAGATGATTCTCCT-----AAGGAGTACACTGACCTAGAAGTATCCAACAAAAG	123
Qy	2865	TGAAATTGCTAATATCCAAAGCGGGCAGATTTCATTGCCTTGCTTAGAATTGCCCTGTGA	2924
Db	124	TGAAATTGCTAATGTCCAGAGCGGGCCAATTTCGTTGCCTTGCTCAGAATTGCCCTGTGA	183
Qy	2925	CCTTTCTTTCAAGAATATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGA	2984
Db	184	CCTTTCTTTCAAGAATACATATCCTAAAGATGAAGCACATGTCTCAGATGAATTCTCCAA	243
Qy	2985	AAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACC	3044
Db	244	AAGTAGGTCCAGTGTATCTAAGGTGCCCTTATTGCTTCCAAATGTTTCTGCTTTGGAATC	303
Qy	3045	TCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAA	3104
Db	304	TCAAATAGAAATGGGCAACATAGTTAAACCCAAAGTACTTACGAAAGAAGCAGAGGAAAA	363
Qy	3105	ACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCT	3164
Db	364	ACTTCCTTCTGATACAGAGAAAGAGGACAGATCCCTGACAGCTGTATTGTCAGCAGAGCT	423
Qy	3165	GAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGT	3224
Db	424	GAATAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGT	483
Qy	3225	GTTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTCAGTGTAAC	3284
Db	484	GTTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTCAGTGTAAC	543
Qy	3285	GGCCTACATTGCCTTGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGT	3344
Db	544	GGCCTACATTGCCTTGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGT	603
Qy	3345	GATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGA	3404

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      ||||| ||||||||||||||||||||||||||||||||||||||| |||||
Db      604 GATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCATATTTGGAATCTGA 663

Qy      3405 AGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAA 3464
      ||||| ||||||||||||||||||||||||||||||||||||||| |||||
Db      664 AGTTGCCATATCAGAGGAATTGGTTCAGAAATATAGTAATTCTGCTCTTGGTCATGTGAA 723

Qy      3465 CAGCACAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAA 3524
      ||||||||||||||| ||||| || |||||||||||||||||||||||
Db      724 CAGCACAATAAAAGAAATTGAGGCGTCTCTTCTTAGTTGATGATTTAGTTGATTCCCTGAA 783

Qy      3525 GTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCC-TTGTTC AATGGTCTGACAC 3583
      | ||||||||||||||| ||||||| ||||||| ||||||| |||||
Db      784 G-TTGCAGTGTTGATGTGGGTATTTACTTACGTTGGTGCCTTTGTTCAATGGTTTGACAC 842

Qy      3584 TACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCC 3620
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Db      843 TACTGATTTTAGCCCTGATCTCACTCTTCAGTATTCC 879

```

RESULT 5

CA504729/c

LOCUS CA504729 796 bp mRNA linear EST 14-NOV-2002

DEFINITION UI-R-FJ0-cpx-e-15-0-UI.s1 UI-R-FJ0 Rattus norvegicus cDNA clone  
UI-R-FJ0-cpx-e-15-0-UI 3', mRNA sequence.

ACCESSION CA504729

VERSION CA504729.1 GI:24995683

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1 (bases 1 to 796)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene  
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: Soares, MB

Coordinated Laboratory for Computational Genomics  
University of Iowa

375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. James Lin, Universtiy of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com).

The following repetitive elements were found in this cDNA  
sequence: 1-35, >POLY\_A#Simple\_repeat (matched compliment)

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES  
source

Location/Qualifiers

1. .796  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clone="UI-R-FJ0-cpx-e-15-0-UI"  
/tissue\_type="embryo"  
/dev\_stage="embryo"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-R-FJ0"  
/note="Vector: pYX-Asc; Site\_1: EcoR I; Site\_2: Not I;  
UI-R-FJ0 is a cDNA library containing the following  
tissue(s): rat embryo. The library was constructed  
according to Bonaldo, Lennon and Soares, Genome Research,  
6:791-806, 1996. First strand cDNA synthesis was primed  
with an oligo-dT primer containing a Not I site. Double  
stranded cDNA was ligated to an EcoR I adaptor, digested  
with Not I, and cloned directionally into pT7T3-Pac  
vector. The oligonucleotide used to prime the synthesis of  
first-strand cDNA contains a library tag sequence that is  
located between the Not I site and the (dT)18 tail. The  
sequence tag for this library is CATCTCTACT. This library  
was created for the University of Iowa Program for Rat  
Gene Discovery and Mapping (Val Sheffield, Bento Soares  
and Tom Casavant)  
TAG\_TISSUE=rat-embryo  
TAG\_LIB=UI-R-FJ0  
TAG\_SEQ=CATCTCTACT"

ORIGIN

Query Match 19.4%; Score 725.6; DB 14; Length 796;  
Best Local Similarity 99.3%; Pred. No. 9.9e-97;  
Matches 728; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 952 TTTAAAGAACATGGATACCTTGGTAACTTATCAGCAGTGTTCATCCTCAGAAGGAACAATT 1011  
|  
Db 733 TCTAAAGAACATGGATACCTTGGTAACTTATCAGCAGTGTTCATCCTCAGAAGGAACAATT 674  
|  
Qy 1012 GAAGAAACTTTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTA 1071  
|  
Db 673 GAAGAACTNTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTA 614  
|  
Qy 1072 AATAGAGATTTAGCAGAATTTTCAGAATTAGAATATTCAGAAATGGGATCATCTTTTAAA 1131  
|  
Db 613 AATAGAGATTTAGCAGAATTTTCAGAATTAGAATATTCAGAAATGGGATCATCTTTTAAA 554  
|  
Qy 1132 GGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAATTGTG 1191  
|  
Db 553 GGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAATTGTG 494  
|  
Qy 1192 AGGAGTAAAGACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCA 1251  
|  
Db 493 AGGAGTAAAGACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCA 434  
|  
Qy 1252 CCTGTGGGTAAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTAATGAA 1311  
|

comprising  
975-1163  
99.3%



Db 433 CCTGTGGGTAAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAA 374

Qy 1312 ATGCAGATGTCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAA 1371  
 |||

Db 373 ATGCAGATGTCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAA 314

Qy 1372 CAAGCATGGGAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT 1431  
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Db 313 CAAGCATGGGAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT 254

Qy 1432 AATGTGGAAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTT 1491  
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Db 253 AATGTGGAAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTT 194

Qy 1492 GGAAGGATAGTGAAGGCAGAAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTG 1551  
 |||

Db 193 GGAAGGATAGTGAAGGCAGAAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTG 134

Qy 1552 AAGGACAGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACC 1611  
 |||

Db 133 AAGGACAGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACC 74

Qy 1612 ACAGCAAACACTTTCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAA 1671  
 |||

Db 73 ACAGCAAACACTTTCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAA 14

Qy 1672 AAAATAGAAGAAA 1684  
 |||

Db 13 AAAAAAAAAAAAAA 1

# RESULT 6

BI730192

LOCUS BI730192 805 bp mRNA linear EST 20-SEP-2001

DEFINITION 603349739F1 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:5357385 5', mRNA sequence.

ACCESSION BI730192

VERSION BI730192.1 GI:15707205

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 805)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: The Cepko Laboratory

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11908 row: n column: 10

High quality sequence stop: 802.

FEATURES  
 source Location/Qualifiers  
 1. .805  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:5357385"  
 /tissue\_type="retina"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_94"  
 /note="Organ: eye; Vector: pCMV-SPORT6; Site\_1: NotI;  
 Site\_2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 3.3 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

# ORIGIN

Query Match 19.0%; Score 709.8; DB 12; Length 805;  
 Best Local Similarity 93.8%; Pred. No. 2.1e-94;  
 Matches 751; Conservative 0; Mismatches 47; Indels 3; Gaps 1;

Qy	1854	AGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGT	1913
Db	1	AGCATGTGAAAGTGAAGTGAACGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGT	60
Qy	1914	GGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTG	1973
Db	61	GGACTTGGTCCAGACATCAGAAGCTATACAAGAGTCAATTTACCCACAGCACAGCTTTG	120
Qy	1974	CCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATGGA	2033
Db	121	CCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATGGA	180
Qy	2034	AGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATC	2093
Db	181	AGCGCCATTAAATTCTCTCCTTCCAAGCACTGGTGCTTCTGTAGCGCAGCCCAGTGCATC	240
Qy	2094	CCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCC	2153
Db	241	CCCACTAGAAGTACCGTCTCCAGTTAGTTATGACGGTATAAAGCTTGAGCCTGAAAATCC	300
Qy	2154	CCCACCATATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAAT	2213
Db	301	CCCACCATATGAAGAAGCCATGAGTGTAGCACTAAAACATCGGACTCAAAGGAAGAAAT	360
Qy	2214	AAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAAGAACAGAAAGCTCCTTATATATCCAT	2273
Db	361	TAAAGAGCCTGAAAGTTTTAATGCAGCTGCTCAGGAAGCAGAAAGCTCCTTATATATCCAT	420
Qy	2274	TGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAA	2333
Db	421	TGCATGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGAGTTCTCTAA	480
Qy	2334	TTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGA	2393
Db	481	TTATTCAGAAATAGCAAAATTTGAGAAGTCGGTGCCCTGATCACTGTGAGCTCGTGGATGA	540

Qy	2394	TTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGT	GATGATT	CGATT	CCTGAAGTCCC	2453
Db	541	TTCCTCACCCGAATCTGAACCAGTTGACTTATTTAGT	GATGATT	CAATTCCTGAAGTCCC	600	
Qy	2454	ACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCT	CACTGAAGTGTCTGAGAC	2513		
Db	601	ACAAACACAAGAGGAGGCTGTGATGCTAATGAAGGAGAGTCT	CACTGAAGTGTCTGAGAC	660		
Qy	2514	AGTAGCCCAGCACAAA---GAGGAGAGACTTAGTGCCCTCACCT	CAGGAGCTAGGAAAGCC	2570		
Db	661	AGTAACACAACACAAACATAAGGAGAGACTTAGTGCTTCACCT	CAGGAGGTAGGAAAGCC	720		
Qy	2571	ATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGAT	GCTGCATCTAATGACAT	2630		
Db	721	ATATTTAGAGTCTTTTCAGCCCAATTTACATATTACCAAAGAT	GCTGCATCTACTGAAAT	780		
Qy	2631	TCCAACATTGACCAAAAAGGA	2651			
Db	781	TCCAACATTGACCAAAAAGGA	801			

CB521332

LOCUS	CB521332	822 bp	mRNA	linear	EST 09-JUL-2003
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DEFINITION UI-M-GH0-cem-h-13-0-UI.r1 NIH\_BMAP\_GH0 Mus musculus cDNA clone  
IMAGE:6841502 5', mRNA sequence.

ACCESSION      CB521332

VERSION CB521332.1 GI:29354687

KEYWORDS EST.

SOURCE      *Mus musculus* (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 822)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT      Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

<http://genome.uiowa.edu/distribution/mousefl.html>

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.

## FEATURES

source

Location/Qualifiers

1. .822

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/organism="Mus musculus"
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/mol type="mRNA"
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/strain="C57BL/6"
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/db xref="taxon:10090"
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/clone="IMAGE:6841502"
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/tissue type="Whole brain"
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```
/dev stage="1, 5, and 15 days newborn"
```

```

/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_GH0"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

```

# ORIGIN

```

Query Match          19.0%;  Score 709.4;  DB 14;  Length 822;
Best Local Similarity 92.6%;  Pred. No. 2.4e-94;
Matches 771;  Conservative 0;  Mismatches 51;  Indels 11;  Gaps 2;

Qy      2762 CTCCGATTGAGATAAATAGATGAATTTCCACGTTTGTGTCAGTGCTAAAGATGATTCTCCTA 2821
      |||| |||||||||||||||||| ||||||| |||||||||||||||||||
Db      1 CTCCCATTGAGATAAATAGATGAGTTTCCACATTGTGTCAGTGCTAAAGATGATTCTCCT- 59

Qy      2822 AATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATCC 2881
      ||||||||||||| ||||||||||| ||||||||||||||||||| |||
Db      60 -----AAGGAGTACACTGACCTAGAAAGTATCCAACAAAAGTGAAATTGCTAATGTCC 111

Qy      2882 AAAGCGGGGCAGATTTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAATA 2941
      | ||||||| ||| ||||||||| |||||||||||||||||||
Db      112 AGAGCGGGGCCAATTCGTTGCCTTGCTCAGAATTGCCCTGTGACCTTTCTTTCAAGAATA 171

Qy      2942 TATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTAT 3001
      ||||||||||||| ||||||| ||| ||||||||| ||| |||||||||
Db      172 CATATCCTAAAGATGAAGCACATGTCTCAGATGAATTCTCCAAAAGTAGGTCCAGTGTAT 231

Qy      3002 CTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGCA 3061
      ||||| || ||| || | ||||||| ||||||||||| ||| | |||||||||
Db      232 CTAAGGTGCCCTTATTGCTTCCAAATGTTTCTGCTTTGGAATCTCAAATAGAAATGGGCA 291

Qy      3062 GCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACAG 3121
      ||||||||| ||||| ||||||||||||||||||| ||||||||||||| ||||
Db      292 ACATAGTTAAACCCAAAGTACTTACGAAAGAAGCAGAGGAAAAAACTTCCTTCTGATACAG 351

Qy      3122 AGAAAGAGGACAGATCCCTGTGCTGCTGATTGTGTCAGCAGAGCTGAGTAAAACTTCAGTTG 3181
      ||||||||||||||||| ||||||||||||||||||| |||||||||||||
Db      352 AGAAAGAGGACAGATCCCTGACAGCTGTATTGTGTCAGCAGAGCTGAATAAACTTCAGTTG 411

Qy      3182 TTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTAT 3241
      ||||||||| ||||||||||||||||||| |||||||||||||
Db      412 TTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTAT 471

Qy      3242 TCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTGTCAGTGTAACGGCCTACATTGCCTTGG 3301
      ||||||||||||||||| |||||||||||||||||||

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Db	472	TCCTGCTGCTGTCTCTGACAGTGTT--TCATTGTCAAGTGTAAACGGCCTACATTGCCTTGG	529
Qy	3302	CCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAGA	3361
Db	530	CCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAAGCTATCCAGA	589
Qy	3362	AATCAGATGAAGGCCACCCATTCAAGGCATATTTAGAATCTGAAGTTGCTATATCAGAGG	3421
Db	590	AATCAGATGAAGGCCACCCATTCAAGGCATATTTGGAATCTGAAGTTGCCATATCAGAGG	649
Qy	3422	AATTGGTTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAGAAC	3481
Db	650	AATTGGTTTCAGAAATATAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAGAAT	709
Qy	3482	TGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCTGAAGTTTGCAGTGTTGATGT	3541
Db	710	TGAGGCGTCTCTTCTTAGTTGATGACTTAGTTGATTCCTGAAGTTTGCAGTGTTGATGT	769
Qy	3542	GGGTGTTTACTTATGTTGGTGCCTTGTTCATGGTCTGACACTACTGATTTTA	3594
Db	770	GGGTATTTACTTACGTTGGTGCCTTGTTCATGGTTTGCACACTACTGACTTTA	822

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/tissue_type="undifferentiated limb"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_134"
/note="Vector: pCMV-SPORT6.1; Site_1: EcoRV; Site_2: NotI;
Cloned unidirectionally. Primer: Oligo dT. Average insert
size 1.7 kb. Constructed by ResGen, Invitrogen Corp. Note:
this is a NIH_MGC Library."

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ORIGIN

```

Query Match          18.9%;  Score 707.8;  DB 13;  Length 986;
Best Local Similarity 87.8%;  Pred. No. 4.1e-94;
Matches 832;  Conservative 0;  Mismatches 103;  Indels 13;  Gaps 5;

Qy      1728 AAATCCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTT 1787
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Db      29 AAATCCTTTCCTTGTAGCAATACATGATTCTGAGGCAGATTATGTCACAACAGATAATTT 88

Qy      1788 ATCAAAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGT 1847
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Db      89 ATCAAAGGTGACTGAGGCAGTAGTGGCAACCATGCCTGAAGGTCTAACGCCAGATTTAGT 148

Qy      1848 TCAGGAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAAC 1907
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Db      149 TCAGGAAGCATGTGAAAGTGAAGTGAACGAAGCCACAGGTACAAAGATTGCTTATGAAAC 208

Qy      1908 AAAAGTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACA 1967
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Db      209 AAAAGTGGACTTGGTCCAGACATCAGAAGCTATACAAGAGTCAATTTACCCACAGCACA 268

Qy      1968 GCTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGT 2027
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Db      269 GCTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGT 328

Qy      2028 TATGGAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAG 2087
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Qy      2088 TGTATCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGA 2147
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Qy      2148 AAACCCCCCACCATATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGA 2207
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Qy      2208 AGGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAACAGAAGCTCCTTATAT 2267
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Db      509 AGAAATTAAAGAGCCTGANAGTTTTAATGCAGCTGCTCAGGAAGCAGAAGCTCCTTATAT 568

Qy      2268 ATCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTT 2327
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Db      569 ATCCATTGCATGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGAGTT 628

Qy      2328 CTCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGT 2387
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Qy	2388	GGAGGATTCTCTCACCTGAATCTGAACCGATTGACTTATTTAGTGATTCGATTCCCTGA	2447
Db	689	GGATGATTCTCTACCCGAATCTGAACCGATTGACTTATTTAGTGATGATTCAATCCCTGA	748
Qy	2448	AGTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTC	2507
Db	749	AGTCCCACCAACACAAGAGGAAGCTGTGATGCTTATGAAAGAGAGTCTCACCTGAATGTC	808
Qy	2508	TGAGACAGTAGCCCAGC----ACAAAGAGGAGAGACTTAGTG----CCTCACCTCAGGAG	2559
Db	809	TGAGACAGTTACCCACCCCAACATAAGGGAGAGACTTAGTGCTTTCCCCTCCGGAGGGT	868
Qy	2560	CTAGGAAAGCCATATTTAGAGTCTTTT--CAGCCCAATTTACATAGT--ACAAAAGATGC	2615
Db	869	AGAAAAGGCCCTATTTTAGAGTCTTTTCAGCCCAATTTACCTATTTACCAAAGGATGC	928
Qy	2616	TGCAT-CTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTT	2662
Db	929	TGCCTCCTAATGAAAATTCACCTTTGGCCCAAAAAGGGAGACCATTTT	976

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/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_HJ0"
/note="Organ: Head; Vector: pYX-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site .Double strand cDNA was
size selected according to mRNA size fraction ,ligated
with EcoR I adaptor , digested with NotI and then cloned
directionally into pYX-Asc vector . The library tag
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
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ORIGIN

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Query Match          18.1%;  Score 678.4;  DB 14;  Length 772;
Best Local Similarity 92.8%;  Pred. No. 8.6e-90;
Matches 725;  Conservative 0;  Mismatches 47;  Indels 9;  Gaps 1;

Qy      2644 AAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAATGAT 2703
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Qy      2704 GACTTACTTTCTTCTAAGGAAGACAAAAATAAAAGAAAGTGAAACATTTTCAGATTCATCT 2763
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Db      61 GACTTACTTTCTTCTAAGGAAGACAAAAATGAAAGAAAGTGAAACATTTTCAGATTCATCT 120

Qy      2764 CCGATTGAGATAATAGATGAATTTCCACGTTTGTGCTGCTAAAGATGATTCTCCTAAA 2823
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Db      121 CCCATTGAGATAATAGATGAGTTTCCACATTTGTGCTGCTAAAGATGATTCTCCT--- 177

Qy      2824 TTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATCCAA 2883
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Db      178 -----AAGGAGTACACTGACCTAGAAGTATCCAACAAAAGTGAAATTGCTAATGTCCAG 231

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Db      232 AGCGGGGCCAATTCGTTGCCTTGCTCAGAATTGCCCTGTGACCTTTCTTTCAAGAATACA 291

Qy      2944 TATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTATCT 3003
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Db      292 TATCCTAAAGATGAAGCACATGTCTCAGATGAATTCTCCAAAAGTAGGTCCAGTGTGTCT 351

Qy      3004 AAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGCAGC 3063
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Db      352 AAGGTGCCCTTATTGCTTCAAATGTTTCTGCTTTGGAATCTCAAATAGAAATGGGCAAC 411

Qy      3064 ATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACAGAG 3123
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Db      412 ATAGTTAAACCCAAAGTACTTACGAAAGAAGCAGAGGAAAAAACTTCCTTCTGATACAGAG 471

Qy      3124 AAAGAGGACAGATCCCTGTGCTGCTGATTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3183
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Db      472 AAAGAGGACAGATCCCTGTGCTGCTGATTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 531
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Qy	3184	GACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTC	3243
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Qy	3244	CTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTGGCC	3303
Db	592	CTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTGGCC	651
Qy	3304	CTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAGAAA	3363
Db	652	CTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCANGCTATCCAGAAA	711
Qy	3364	TCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAGGAA	3423
Db	712	TCAGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGGCATATCAGAGGAA	771
Qy	3424	T	3424
Db	772	T	772





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/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FW0"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

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ORIGIN

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Query Match          17.7%;  Score 662.6;  DB 14;  Length 777;
Best Local Similarity 92.1%;  Pred. No. 1.8e-87;
Matches 724;  Conservative 0;  Mismatches 50;  Indels 12;  Gaps 2;

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Qy      2147 AAAACCCCCCACCATATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGG 2206
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Db      1 AAAATCCCCCACCATATGAAGAAGCCATGAGTGTAGCACTAAAACATCGGACTCAAAGG 60

Qy      2207 AAGGAATAAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATA 2266
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Db      61 AAGAAATTAAGAGCCTGAAAGTTTTAATGCAGCTGCTCAGGAAGCAGAAGCTCCTTATA 120

Qy      2267 TATCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATT 2326
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Qy      2327 TCTCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAG 2386
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Db      181 TCTCTAATTATTCAGAAATAGCAAAATTTGAGAAGTCGGTGCCCTGATCACTGTGAGCTCG 240

Qy      2387 TGGAGGATTCCCTCACCTGAATCTGAACCAAGTTGACTTATTTAGTGATGATTCGATTCCTG 2446
      |||| ||||||| ||||||||||||||||||||||||||| |||||||
Db      241 TGGATGATTCCCTCACCCGAATCTGAACCAAGTTGACTTATTTAGTGATGATTCGAATTCCTG 300

Qy      2447 AAGTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGT 2506
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Qy      2507 CTGAGACAGTAGCCCAGCACAAA---GAGGAGAGACTTAGTGCCCTCACCTCAGGAGCTAG 2563
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Db      361 CTGAGACAGTAACACAACACAACATAAGGAGAGACTTAGTGCTTCACCTCAGGAGGTAG 420

Qy      2564 GAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTA 2623
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Db      421 GAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATATTACAAAAGATGCTGCATCTA 480

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Db	541	CTGCAATTTTATTCCAATGATGACTTACTTTCTTCTAAGGAAGACAAAATGAAAGAAAGTG	600
Qy	2744	AAACATTTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTGTCAGTG	2803
Db	601	AAACATTTTTCGATTTCATCTCTCATTGAGATAATAGATGAGTTTCCACATTTGTGTCAGTG	660
Qy	2804	CTAAAGATGATTCTCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAA	2863
Db	661	CTAAAGATGATTCTCCT-----AAGGAGTACACTGACCTAGAAGTATCCAACAAAA	711
Qy	2864	GTGAAATTGCTAATATCCAAAGCGGGGCAGATTTCATTGCCTTGCTTAGAATTGCCCTGTG	2923
Db	712	GTGAAATTGCTAATGTCCAGAGCGGNGGCAATTCGTTGCCTTGCTCAGAATTGCCCTGTG	771
Qy	2924	ACCTTT	2929
Db	772	ACCTTT	777

CA320635

LOCUS	CA320635	802 bp	mRNA	linear	EST 09-JUL-2003
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DEFINITION UI-M-FW0-ccb-o-24-0-UI.r1 NIH\_BMAP\_FW0 Mus musculus cDNA clone  
IMAGE:6817489 5', mRNA sequence.

ACCESSION CA320635

VERSION CA320635.1 GI:24538759

KEYWORDS EST.

SOURCE      Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 802)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT      Contact: Robert Strausberg, Ph.D.

Email: [cqapbs-r@mail.nih.gov](mailto:cqapbs-r@mail.nih.gov)

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.

FEATURES	Location/Qualifiers
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/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

```

# ORIGIN

```

Query Match          17.7%;  Score 660.4;  DB 14;  Length 802;
Best Local Similarity 91.6%;  Pred. No. 3.8e-87;
Matches 745;  Conservative 0;  Mismatches 54;  Indels 14;  Gaps 4;

Qy      2148 AAACCCCCCACCATATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGA 2207
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Db      241 GGATGATTTCCTCACCCGAATCTGAACCAAGTTGACTTATTTAGTGATGATTCAATTTCCTGA 300

Qy      2448 AGTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTC 2507
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Db	421	AAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATATTACAAAAGATGCTGCATCTAA	480
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Qy	2685	TGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGA	2744
Db	541	TGCAATTTATTCCAATGATGACTTACTTTCTTCTAAGGAAGACAAAATGAAAGAAAGTGA	600
Qy	2745	AACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTCAGTGC	2804
Db	601	AACATTTTCAGATTTCATCTCNCATTGAGATAATAGATGAGTTTCNCACATTTGTCAGTGC	660
Qy	2805	TAAAGATGATTCTCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAG	2864
Db	661	TAAAGATGATTCTCCT-----AAGGAGTACACTGACCTAGAAGTATCCAACACAAG	711
Qy	2865	TGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTGCCCTGTGA	2924
Db	712	TGAAATTGCTAATGTCCAGAGCGGGGCCAATTCGTTGCCTTGCTCAGATTTG-CCTGTGA	770
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Primer: Oligo dT. Average insert size 2.2 kb. Constructed
by ResGen, Invitrogen Corp. Note: this is a NIH_MGC
Library."

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# ORIGIN

```

Query Match          17.6%;  Score 659.2;  DB 13;  Length 951;
Best Local Similarity 89.3%;  Pred. No. 5.7e-87;
Matches 780;  Conservative 0;  Mismatches 79;  Indels 14;  Gaps 6;

Qy      2646 AAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAATGATGA 2705
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Qy 3246 GCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAAACGGCCTACATTG-CCTTGGCCC 3304  
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 Qy 3424 TTGG-TTCAGAAATACA-GTAATTCTGCTCTTGGTCATGTGAACAG-CACAATAAAAGAA 3480  
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 Db 782 TTGGTTTCAGAAATATAGGAAATCTGCTCTTGGGCATGGGGACCGCCACAATAAAAGAA 841  
 Qy 3481 CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTT 3513  
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 Db 842 ATGGAGGGGTCTCCTCCTAAGTTAATGGATTT 874

#### RESULT 14

CF726835

LOCUS CF726835 767 bp mRNA linear EST 09-OCT-2003

DEFINITION UI-M-HB0-cki-m-06-0-UI.r1 NIH\_BMAP\_HB0 Mus musculus cDNA clone  
 IMAGE:30548549 5', mRNA sequence.

ACCESSION CF726835

VERSION CF726835.1 GI:37601003

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 767)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Dr. James Lin University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

<http://genome.uiowa.edu/distribution/mousefl.html>

This clone was contributed by the Brain Molecular Anatomy Project  
 (BMAP)

Seq primer: pYX-5.

#### FEATURES

source

Location/Qualifiers

1. .767

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6"

/db\_xref="taxon:10090"

/clone="IMAGE:30548549"

/tissue\_type="whole eye"

/dev\_stage="embryo 12.5,13.5,14.5 dpc"

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/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_HB0"
/note="Organ: Eye; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site .Double strand cDNA was
size selected according to mRNA size fraction ,ligated
with EcoR I adaptor , digested with NotI and then cloned
directionally into pYX-Asc vector . The library tag
sequence located between the Not I site and the polyA tail
is TTATTGAAGT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
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# ORIGIN

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Query Match          17.4%;  Score 651.2;  DB 14;  Length 767;
Best Local Similarity 93.4%;  Pred. No. 8.5e-86;
Matches 718;  Conservative 0;  Mismatches 34;  Indels 17;  Gaps 3;
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Qy      890 CATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTT 949
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 Db 720 TGGAGC-NAAAGGTCATGGGAAGGATAGTGAAGGCAGAAATGAGAATGC 767

RESULT 15

BU612951

LOCUS BU612951 739 bp mRNA linear EST 20-FEB-2003

DEFINITION UI-M-FR0-cbd-a-04-0-UI.r1 NIH\_BMAP\_FR0 Mus musculus cDNA clone  
 UI-M-FR0-cbd-a-04-0-UI 5', mRNA sequence.

ACCESSION BU612951

VERSION BU612951.1 GI:23279166

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 739)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained  
 from Dr. M. Bento Soares, [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)

This clone was contributed by the Brain Molecular Anatomy Project  
 (BMAP)

Seq primer: pYX-5.

FEATURES

source

Location/Qualifiers

1. .739

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6"

/db\_xref="taxon:10090"

/clone="UI-M-FR0-cbd-a-04-0-UI"

/tissue\_type="whole brain"

/dev\_stage="embryo 13.5,14.5,16.5,17.5dpc"

/lab\_host="DH10B (T1 phage resistant)"

/clone\_lib="NIH\_BMAP\_FR0"

/note="Organ: Brain; Vector: pYX- Asc; Site\_1: EcoR I;

Site\_2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

# ORIGIN

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Query Match          17.3%;  Score 648.6;  DB 13;  Length 739;
Best Local Similarity 92.9%;  Pred. No. 2e-85;
Matches 694;  Conservative 0;  Mismatches 44;  Indels 9;  Gaps 1;

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Db      62   TGAGTTTCCCACATTTGTCTAGTGCTAAAGATGATTCTCTCT-----AAGGAGTACAC 112

Qy      2841 TGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTTCATT 2900
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Qy      2901 GCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAGT 2960
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Qy      2961 ACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCC 3020
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Db      293  TCCAAATGTTTCTGCTTTGGAATCTCAAATAGAAATGGGCAACATAGTTAAACCCAAAGT 352

Qy      3081 ACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCT 3140
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Qy      3141 GTCAGCTGTATTGTCTAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTCTACTGGAG 3200
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Qy      3201 AGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGAC 3260
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Qy      3261 AGTGTTCAGCATTGTCTAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTAT 3320

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Qy      3321 CAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCC 3380
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Db      593 CAGCTTTAGGATATATAAGGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCC 652
Qy      3381 ATTCAGGGCATATTTAGAACTCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAG 3440
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Db      653 ATTCAGGGCATATTTGGAATCTGAAGTTGCCATATCAGAGGAATTGGTTCAGAAATATAG 712
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Db      713 TAATTCTGCTCTTGGTCATGTGAACAG 739

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Search completed: September 11, 2004, 15:09:45  
Job time : 8884.33 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 00:39:35 ; Search time 14076.4 Seconds  
(without alignments)  
11519.006 Million cell updates/sec

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Perfect score: 3741  
Sequence: 1 attgctcgtctggcgccgg.....gattgaagcgcaaagcagat 3741

Scoring table: IDENTITY\_NUC  
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Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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	3	3202.4	85.6	4627	10	AY102284	AY102284 Mus muscu
	4	3200.4	85.5	3821	10	AY114152	AY114152 Mus muscu
	5	3140.4	83.9	4518	10	BC056373	BC056373 Mus muscu
	6	2651	70.9	4063	10	AY102280	AY102280 Mus muscu
	7	2543.6	68.0	3815	10	BC032272	BC032272 Mus muscu
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	9	2391.4	63.9	4789	9	AY102279	AY102279 Homo sapi
	10	2353.8	62.9	218532	2	AC131431	AC131431 Rattus no
	11	2353.8	62.9	238341	2	AC133315	AC133315 Rattus no
	12	2343.6	62.6	4053	6	AX195249	AX195249 Sequence
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	14	2343.6	62.6	4632	9	AF148537	AF148537 Homo sapi
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	22	2062	55.1	211357	2	AC113284	AC113284 Mus muscu
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	24	2011	53.8	4102	9	AY123245	AY123245 Homo sapi
	25	2009.8	53.7	4123	9	AY123247	AY123247 Homo sapi
	26	2009.6	53.7	4070	9	AY123249	AY123249 Homo sapi
	27	2008.6	53.7	3491	9	AF333336	AF333336 Homo sapi
	28	2008.6	53.7	4109	9	AY123248	AY123248 Homo sapi
	29	2007.6	53.7	4060	9	AY123250	AY123250 Homo sapi
	30	2007.6	53.7	4160	9	AY123246	AY123246 Homo sapi
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	32	1769.4	47.3	2883	9	AF320999	AF320999 Homo sapi
	33	1541.2	41.2	1738	10	AB073672	AB073672 Mus muscu

	34	1486.6	39.7	2481	9	AF063601	AF063601 Homo sapi
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# ALIGNMENTS

## RESULT 1

RNO242961

LOCUS RNO242961 4684 bp mRNA linear ROD 28-JAN-2000

DEFINITION Rattus norvegicus mRNA for Nogo-A protein.

ACCESSION AJ242961

VERSION AJ242961.1 GI:6822246

KEYWORDS Nogo-A protein.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

## REFERENCE 1

AUTHORS Chen,M.S., Huber,A.B., van der Haar,M.E., Frank,M., Schnell,L.,  
Spillmann,A.A., Christ,F. and Schwab,M.E.

TITLE Nogo-A is a myelin-associated neurite outgrowth inhibitor and an  
antigen for monoclonal antibody IN-1

JOURNAL Nature 403 (6768), 434-439 (2000)

MEDLINE 20129258

PUBMED 10667796

## REFERENCE 2 (bases 1 to 4684)

AUTHORS Van der Haar,M.E.

TITLE Direct Submission

JOURNAL Submitted (14-JUN-1999) Van der Haar M.E., Department of  
Neuromorphology, Brain Research Institute, University of Zurich,  
Winterthurerstrasse 190, Zurich, CH-8057, SWITZERLAND

## FEATURES

Location/Qualifiers

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/mol\_type="mRNA"  
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gene

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CDS

253. .3744  
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# ORIGIN

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Query Match          100.0%;  Score 3739.4;  DB 10;  Length 4684;
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Qy    361  GACGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTG  420
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Qy	481	CCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCC	540
Db	481	CCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCC	540
Qy	541	GCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCG	600
Db	541	GCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCG	600
Qy	601	CCATCCCTGCCGCGCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCT	660
Db	601	CCATCCCTGCCGCGCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCT	660
Qy	661	CCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCG	720
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Qy	721	CCCCCTTCCACGCCGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTT	780
Db	721	CCCCCTTCCACGCCGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTT	780
Qy	781	TTTGCTCTTCCTGCTGCATCTGAGCCTGTGATAACCCTCCTCTGCAGAAAAAATTATGGAT	840
Db	781	TTTGCTCTTCCTGCTGCATCTGAGCCTGTGATAACCCTCCTCTGCAGAAAAAATTATGGAT	840
Qy	841	TTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTG	900
Db	841	TTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTG	900
Qy	901	CTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAA	960
Db	901	CTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAA	960
Qy	961	CATGGATACCTTGGTAACTTATCAGCAGTGTATCCTCAGAAGGAACAATTGAAGAAACT	1020
Db	961	CATGGATACCTTGGTAACTTATCAGCAGTGTATCCTCAGAAGGAACAATTGAAGAAACT	1020
Qy	1021	TTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGAT	1080
Db	1021	TTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGAT	1080
Qy	1081	TTAGCAGAATTTTCAGAATTAGAATATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCA	1140
Db	1081	TTAGCAGAATTTTCAGAATTAGAATATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCA	1140
Qy	1141	AAAGGAGAGTCAGCCATATTAGTAGAAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA	1200
Db	1141	AAAGGAGAGTCAGCCATATTAGTAGAAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA	1200
Qy	1201	GACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCTGTGGGT	1260
Db	1201	GACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCTGTGGGT	1260
Qy	1261	AAAGAAGACAGAGTTGTGTCTCCAGAAAAACAATGGACATTTTAAATGAAATGCAGATG	1320

Db	1261	 AAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATG	1320
Qy	1321	TCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGG	1380
Db	1321	 TCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGG	1380
Qy	1381	GAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTGGAA	1440
Db	1381	 GAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTGGAA	1440
Qy	1441	AGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGAAGGAT	1500
Db	1441	 AGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGAAGGAT	1500
Qy	1501	AGTGAAGGCAGAAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGACAGC	1560
Db	1501	 AGTGAAGGCAGAAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGACAGC	1560
Qy	1561	TCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACAGCAAAC	1620
Db	1561	 TCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACAGCAAAC	1620
Qy	1621	ACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAAATAGAA	1680
Db	1621	 ACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAAATAGAA	1680
Qy	1681	GAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTCCCTT	1740
Db	1681	 GAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTCCCTT	1740
Qy	1741	GTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACT	1800
Db	1741	 GTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACT	1800
Qy	1801	GAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGCATGT	1860
Db	1801	 GAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGCATGT	1860
Qy	1861	GAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTG	1920
Db	1861	 GAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTG	1920
Qy	1921	GTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTGCCCATCA	1980
Db	1921	 GTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTGCCCATCA	1980
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Db	1981	 TTTGAGGAAGCTGAAGCAACTCCGTCAACAGTTTTGCCTGATATTGTTATGGAAGCACCA	2040
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Db	2041	 TTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCACTG	2100
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Db	2101	GAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCACCA	2160
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Qy	2221	CCTGAAAGTTTAAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGT	2280
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Db	2281	GATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTCA	2340
Qy	2341	GAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCCCTCA	2400
Db	2341	GAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCCCTCA	2400
Qy	2401	CCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCTGAAGTCCCACAAACA	2460
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Qy	2461	CAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCC	2520
Db	2461	CAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCC	2520
Qy	2521	CAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAGCCATATTTAGAG	2580
Db	2521	CAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAGCCATATTTAGAG	2580
Qy	2581	TCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTG	2640
Db	2581	TCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTG	2640
Qy	2641	ACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAAT	2700
Db	2641	ACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAAT	2700
Qy	2701	GATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCA	2760
Db	2701	GATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCA	2760
Qy	2761	TCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTGCTAGTGCTAAAGATGATTCTCCT	2820
Db	2761	TCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTGCTAGTGCTAAAGATGATTCTCCT	2820
Qy	2821	AAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATC	2880
Db	2821	AAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATC	2880
Qy	2881	CAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAAT	2940
Db	2881	CAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAAT	2940
Qy	2941	ATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTA	3000
Db	2941	ATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTA	3000

Qy	3001	TCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGC	3060
Db	3001	TCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGC	3060
Qy	3061	AGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACA	3120
Db	3061	AGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACA	3120
Qy	3121	GAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACCTTCAGTT	3180
Db	3121	GAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACCTTCAGTT	3180
Qy	3181	GTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTA	3240
Db	3181	GTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTA	3240
Qy	3241	TTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTG	3300
Db	3241	TTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTG	3300
Qy	3301	GCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAG	3360
Db	3301	GCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAG	3360
Qy	3361	AAATCAGATGAAGGCCACCCATTTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAG	3420
Db	3361	AAATCAGATGAAGGCCACCCATTTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAG	3420
Qy	3421	GAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAGAA	3480
Db	3421	GAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAGAA	3480
Qy	3481	CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATG	3540
Db	3481	CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATG	3540
Qy	3541	TGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTG	3600
Db	3541	TGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTG	3600
Qy	3601	ATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTAT	3660
Db	3601	ATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTAT	3660
Qy	3661	CTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCT	3720
Db	3661	CTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCT	3720
Qy	3721	GGATTGAAGCGCAAAGCAGAT	3741
Db	3721	GGATTGAAGCGCAAAGCAGAT	3741

RESULT 2  
AX766046  
LOCUS

AX766046

3489 bp

DNA

linear

PAT 25-JUN-2003

DEFINITION Sequence 1 from Patent WO03002602.  
 ACCESSION AX766046  
 VERSION AX766046.1 GI:32260128  
 KEYWORDS .  
 SOURCE Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 REFERENCE 1  
 AUTHORS Eisenbach-Schwartz,M. and Hauben,E.  
 TITLE Nogo and nogo receptor derived peptides for t-cell mediated  
 neuroprotection  
 JOURNAL Patent: WO 03002602-A 1 09-JAN-2003;  
 YEDA RESEARCH AND DEVELOPMENT Co. LTD. (IL)  
 FEATURES Location/Qualifiers  
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 /db\_xref="taxon:10116"  
 exon 1. .3489  
 ORIGIN

Query Match 93.3%; Score 3489; DB 6; Length 3489;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	253	ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCT	312
Db	1	ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCT	60
Qy	313	CCGCCCCGCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG	372
Db	61	CCGCCCCGCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG	120
Qy	373	GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG	432
Db	121	GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG	180
Qy	433	CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCGCCGCCGCTGCTGGAC	492
Db	181	CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCGCCGCCGCTGCTGGAC	240
Qy	493	TTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCCCCTGCC	552
Db	241	TTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCCCCTGCC	300
Qy	553	GCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCGCCATCCTGCCG	612
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Qy	613	CCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCTCCGGCGAGGCCC	672
Db	361	CCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCTCCGGCGAGGCCC	420
Qy	673	CCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCCGCCCTTCCACG	732

Db	421	CCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCGCCCCCTTCCACG	480
Qy	733	CCGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTTTTGTCTTCCT	792
Db	481	CCGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTTTTGTCTTCCT	540
Qy	793	GCTGCATCTGAGCCTGTGATACCCTCCTCTGCAGAAAAAATTATGGATTGATGGAGCAG	852
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Qy	853	CCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCT	912
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Qy	913	GCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTT	972
Db	661	GCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTT	720
Qy	973	GGTAACTTATCAGCAGTGTCTATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCT	1032
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Qy	1033	TCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTGTAAATAGAGATTTAGCAGAATTT	1092
Db	781	TCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTGTAAATAGAGATTTAGCAGAATTT	840
Qy	1093	TCAGAATTAGAATATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCA	1152
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Qy	1213	TTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCTGTGGGTAAAGAAGACAGA	1272
Db	961	TTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCTGTGGGTAAAGAAGACAGA	1020
Qy	1273	GTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTAGCA	1332
Db	1021	GTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTAGCA	1080
Qy	1333	CCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAAGAT	1392
Db	1081	CCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAAGAT	1140
Qy	1393	ACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTGGAAAGTAAAGTGGAC	1452
Db	1141	ACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTGGAAAGTAAAGTGGAC	1200
Qy	1453	AGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGAAGGATAGTGAAGGCAGA	1512
Db	1201	AGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGAAGGATAGTGAAGGCAGA	1260
Qy	1513	AATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGACAGCTCCAGAGCATAT	1572
Db	1261	AATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGACAGCTCCAGAGCATAT	1320

Qy	1573	ATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACAGCAAACACTTTCCCTTTG	1632
Db	1321	ATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACAGCAAACACTTTCCCTTTG	1380
Qy	1633	TTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAAATAGAAGAAAGGAAGGCC	1692
Db	1381	TTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAAATAGAAGAAAGGAAGGCC	1440
Qy	1693	CAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTCCTTGTAGCAGTACAG	1752
Db	1441	CAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTCCTTGTAGCAGTACAG	1500
Qy	1753	GATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACTGAGGCAGCAGTG	1812
Db	1501	GATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACTGAGGCAGCAGTG	1560
Qy	1813	TCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGCATGTGAAAGTGAAGT	1872
Db	1561	TCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGCATGTGAAAGTGAAGT	1620
Qy	1873	AATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTGGTCCAAACATCA	1932
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Qy	1933	GAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTGCCCATCATTTGAGGAAGCT	1992
Db	1681	GAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTGCCCATCATTTGAGGAAGCT	1740
Qy	1993	GAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATGGAAGCACCATTAAATTCTCTC	2052
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Qy	2053	CTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCACTGGAAGCACCTCCT	2112
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Qy	2113	CCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCACCATATGAAGAAGCC	2172
Db	1861	CCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCACCATATGAAGAAGCC	1920
Qy	2173	ATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAGCCTGAAAGTTTT	2232
Db	1921	ATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAGCCTGAAAGTTTT	1980
Qy	2233	AATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGTGATTTAATTAAA	2292
Db	1981	AATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGTGATTTAATTAAA	2040
Qy	2293	GAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTTCAGAAATAGCAAAA	2352
Db	2041	GAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTTCAGAAATAGCAAAA	2100
Qy	2353	TTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCTCACCTGAATCTGAA	2412
Db	2101	TTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCTCACCTGAATCTGAA	2160



Qy	2413	CCAGTTGACTTATTTAGTGATGATTCGATTCTGAAGTCCCACAAACACAAGAGGAGGCT	2472
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Qy	2473	GTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCCCAGCACAAAGAG	2532
Db	2221	GTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCCCAGCACAAAGAG	2280
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Qy	2593	AATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTGACCAAAAAGGAG	2652
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Qy	2713	TCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAG	2772
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Qy	2893	GATTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAATATATATCCTAAA	2952
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Qy	3133	AGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTC	3192
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Qy	3193	TACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTG	3252
Db	2941	TACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTG	3000
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Db      3001  |||||TCTCTGACAGTGTTCAGCATTGTCAGTGTAAACGGCCTACATTGCCCTGGCCCTGCTCTCG 3060
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Db      3061  |||||GTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAA 3120
Qy      3373  GGCCACCCATTTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAG 3432
Db      3121  |||||GGCCACCCATTTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAG 3180
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Db      3181  |||||AAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAAATAAAAGAACTGAGGCGGCTT 3240
Qy      3493  TTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACT 3552
Db      3241  |||||TTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACT 3300
Qy      3553  TATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTC 3612
Db      3301  |||||TATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTC 3360
Qy      3613  AGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCA 3672
Db      3361  |||||AGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCA 3420
Qy      3673  AACAAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGC 3732
Db      3421  |||||AACAAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGC 3480
Qy      3733  AAAGCAGAT 3741
Db      3481  |||||AAAGCAGAT 3489

```

### RESULT 3

AY102284

LOCUS AY102284 4627 bp mRNA linear ROD 29-JAN-2003

DEFINITION Mus musculus RTN4 (Rtn4) mRNA, complete cds, alternatively spliced.

ACCESSION AY102284

VERSION AY102284.1 GI:23379816

KEYWORDS .

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 4627)

AUTHORS Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.

TITLE Genomic Structure and Functional Characterisation of the Promoters  
of Human and Mouse nogo/rtn4

JOURNAL J. Mol. Biol. 325 (2), 299-323 (2003)

MEDLINE 22376540

PUBMED 12488097

REFERENCE 2 (bases 1 to 4627)

AUTHORS Oertle,T. and Schwab,M.E.

TITLE Direct Submission

JOURNAL Submitted (07-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057, Switzerland

REFERENCE 3 (bases 1 to 4627)

AUTHORS Van der Putten,H.

TITLE Direct Submission

JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma Inc., Basel, Switzerland

FEATURES Location/Qualifiers

source	1. .4627 /organism="Mus musculus" /mol_type="mRNA" /strain="129/SvcJ7" /db_xref="taxon:10090" /chromosome="11"
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5'UTR	1. .248 /gene="Rtn4"
CDS	249. .3737 /gene="Rtn4" /note="NOGO-A; RTN4-A; alternatively spliced" /codon_start=1 /product="RTN4" /protein_id="AAM73506.1" /db_xref="GI:23379817" /translation="MEDIDQSSLVSSSADSPPRPPPAFKYQFVTEPEDEEDEDEDEDEE EDEDELEELVLERKPAAGLSAAPVPPAAAPLLDFSSDSVPPAPRGPLPAAPPPTAPER QPSWERSPAASAPSLPPAAAVLP SKLPEDDEPPARPPAPAGASPLAEPAAAPPSTPAAP KRRGSGSVDETLEFALPAASEPVIPSSAEKIMDLKEQPGNTVSSGQEDFPSVLFFETAAS LPSLSPLSTVSFKEHGYLGNL SAVASTEGTIEETLINEASRELPERATNPFVNRESAEF SVLEYSEMGSFNGSPKGESAMLVENTKEEVIVRSKDKEDLVCSAALHNPQESPATLT KVKEDGVM SPEKTMDIFNEMKMSV VAPVREEYADFKPFEQAWEVKDTYEGSRDVLAA RANMESKVDKKCFEDSLEQKGHGKDSERNENASFPRTPELVKDGSRAYITCDSFSSA TESTAANIFPVLEDHTSENKTDEKKIEERKAQIITEKTSPKTSNPFVLAHIDSEADYV TTDNLSKVTEAVVATMP EGLTPDLVQEACESELNEATGTKIAYETKVDLVQTS EAIQE SIYPTAQLCP SFEEAEATPSPVLPDIVMEAPLNSLLPSTGASVAQPSASPLEVPSPV YDGIKLEPENPPPYEEAMSVALKTSDSKEEIKEPESFNAAQAEAPYISIACDLIKE TKLSTEPSPEFSNYSEIAKFEKSVDPDHCELVDSSPESEPVDLFSDDSIPEVPQTQEE AVMLMKESL TEVSETVTQHKKERLSASPQEVGKPYLESFQPNLHITKDAASNEIPTL TKKETISLQMEEFNTAIYSNDDLSSKEDKMKESETFSDSSPIEIIDFPTFVSAKDD SPKEYTDLEVS NKSEIANVQSGANSLPCSELPCDLSFKNTYPKDEAHVSDEF SKSRSS VSKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEEKLP SDTEKEDRSLTAVLSAELNK TSVVDLLYWRDIKKTGVVFGASL FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDL VDS LKFAVLMWVFETYVGALENGLTLL LILALISLFSIPVIYERHQAQIDHYLGLANKSVKDA MAKIQAKIPGLKRKAE"
3'UTR	3738. .4627 /gene="Rtn4"

ORIGIN

Query Match 85.6%; Score 3202.4; DB 10; Length 4627;  
Best Local Similarity 92.8%; Pred. No. 0;  
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Qy	61	ATCGCGAAGGCAGCAGAAGCAGTCTCATTGTTCCGGGAGCCGTGCGCTCTGCAGGTTCTT	120
Db	76	AGCGCGGAGGCAGGAGGAGAAGTCTTATTGTTCTGAGCTGTGCGCTTTGCGGGTTCCT	135
Qy	121	CGGCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACA	180
Db	136	CGGCTTGG-----TTCGGCCAGCCCGGCTCTGCCAGTCTTGCCCAACCCCCACA	185
Qy	181	ACCGCCCGCGACTCTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGC	240
Db	186	ACCGCCCGCGGCTCTGAGGAGAAGTGCCCC-GCGGCGGCAGTAGCTGCAGCATCATCGCC	244
Qy	241	GACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGC	300
Db	245	GA-----CCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCGCGGATAGC	296
Qy	301	CCGCCCCGGCCTCCGCCCCGCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAG	360
Db	297	CCGCCCCGGCCCCCGCCCCGCTTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAG	356
Qy	361	GACGAGGAGGAGGAGGAGGAGACGAGGAGGAGGACGACGAGGACCTAGAGGAACGGAGGTG	420
Db	357	GACGAGGAAGACGAGGAG---GAGGAGGAGGACGACGAGGACCTGGAGGAATTGGAGGTG	413
Qy	421	CTGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCCGCG	480
Db	414	CTGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCAGGCTCCGGT---GCCGCCCGCCGCCGCA	470
Qy	481	CCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCCGGGCCGCTGCCGGCC	540
Db	471	CCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCCGGGCCGCTGCCGGCC	530
Qy	541	GCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCG	600
Db	531	GCGCCCCCACCGCCCCCTGAGAGGCAGCCGTCTGGGAACGCAGCCCCGCGGCGTCCGCG	590
Qy	601	CCATCCCTGCCGCCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCT	660
Db	591	CCATCCCTGCCGCCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCGAGGACGACGAGCCT	650
Qy	661	CCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCG	720
Db	651	CCAGCG-----CGGCCTCCGGCGCCAGCCGGCGCGAGCCCCCTAGCGGAGCCCGCCGCG	704
Qy	721	CCCCCTTCCACGCCGGCCGCGCCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTT	780
Db	705	CCCCCTTCCACGCCGGCCGCGCCCCAAGCGCAGGGGCTCGGGCTCAGTGGATGAGACCCTT	764
Qy	781	TTTGCTCTTCCTGCTGCATCTGAGCCTGTGATACCCTCCTCTGCAGAAAAAATTATGGAT	840
Db	765	TTTGCTCTTCCTGCTGCATCTGAGCCTGTGATACCCTCCTCTGCAGAAAAAATTATGGAT	824
Qy	841	TTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTG	900

Db 825 TTGAAGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCTCATCTGTCCTG 884  
 Qy 901 CTTGAAACTGCTGCCTCTCTTCCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAA 960  
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 Db 885 TTTGAAACTGCTGCCTCTCTTCCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAA 944  
 Qy 961 CATGGATACCTTGGTAACTTATCAGCAGTGTCTATCCTCAGAAGGAACAATTGAAGAACT 1020  
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 Db 945 CACGGATACCTTGGTAACTTATCAGCAGTGGCATCCACAGAAGGAACATTGAAGAACT 1004  
 Qy 1021 TTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGAT 1080  
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 Db 1005 TTAAATGAAGCTTCTAGAGAATTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGAG 1064  
 Qy 1081 TTAGCAGAAATTTTCAGAAATAGAATATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCA 1140  
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 Db 1065 TCAGCAGAGTTTTCAGTATTAGAATACTCAGAAATGGGATCATCTTTCAATGGCTCCCCA 1124  
 Qy 1141 AAAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA 1200  
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 Db 1125 AAAGGAGAGTCAGCCATGTTAGTAGAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA 1184  
 Qy 1201 GACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCT----- 1254  
 |||||  
 Db 1185 GACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCATAATCCACAAGAGTCACCTGCGACC 1244  
 Qy 1255 -----GTGGGTAAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTT 1305  
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 Db 1245 CTTACTAAAGTGTTTAAAGAAGACGGAGTTATGTCTCCAGAAAAGACAATGGACATTTTTT 1304  
 Qy 1306 AATGAAATGCAGATGTCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCA 1365  
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 Db 1305 AATGAAATGAAATGTCAGTGGTAGCACCTGTGAGGGAAGAGTATGCAGATTTTAAAGCCA 1364  
 Qy 1366 TTTGAACAAGCATGGGAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCT 1425  
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 Db 1365 TTTGAACAAGCATGGGAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCT 1424  
 Qy 1426 AGAGCTAATGTGGAAAGTAAAGTGGACAGAAAATGCTTGGAAAGATAGCCTGGAGCAAAAA 1485  
 |||||  
 Db 1425 AGAGCTAATATGGAAAGTAAAGTGGACAAAAAATGCTTTGAAGATAGCCTGGAGCAAAAA 1484  
 Qy 1486 AGTCTTGGGAAGGATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAA 1545  
 |||||  
 Db 1485 GGTCTATGGGAAGGATAGTGAAGGCAGAAATGAGAATGCTTCTTTCCCCAGGACCCAGAA 1544  
 Qy 1546 CCTGTGAAGGACAGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAA 1605  
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 Db 1545 CTTGTGAAGGACGGCTCCAGAGCGTACATCACCTGTGATTTCCTTTAGCTCAGCAACCGAG 1604  
 Qy 1606 AGCACCACAGCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAACAGAT 1665  
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 Db 1605 AGTACTGCAGCAAACATTTCCCTGTGCTAGAAGATCACACTTCAGAAAACAAAACAGAT 1664  
 Qy 1666 GAAAAAAAAAATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACG 1725  
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 Db 1665 GAAAAAAAAAATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACG 1724

Qy	1726	TCAAATCCTTTCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACC	1785
Db	1725	TCAAATCCTTTCTTGTAGCAATACATGATTCTGAGGCAGATTATGTCACAACAGATAAT	1784
Qy	1786	TTATCAAAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTA	1845
Db	1785	TTATCAAAGGTGACTGAGGCAGTAGTGGCAACCATGCCTGAAGGTCTAACGCCAGATTTA	1844
Qy	1846	G TTCAGGAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAA	1905
Db	1845	G TTCAGGAAGCATGTGAAAGTGAAGTGAACGAAGCCACAGGTACAAAGATTGCTTATGAA	1904
Qy	1906	ACAAAAGTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCA	1965
Db	1905	ACAAAAGTGGACTTGGTCCAGACATCAGAAGCTATACAAGAGTCAATTTACCCACAGCA	1964
Qy	1966	CAGCTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATT	2025
Db	1965	CAGCTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATT	2024
Qy	2026	GTTATGGAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCC	2085
Db	2025	GTTATGGAAGCGCCATTAAATTCTCTCCTTCCAAGCACTGGTGCTTCTGTAGCGCAGCCC	2084
Qy	2086	AGTGTATCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCT	2145
Db	2085	AGTGCATCCCCACTAGAAGTACCGTCTCCAGTTAGTTATGACGGTATAAAGCTTGAGCCT	2144
Qy	2146	GAAAACCCCCACCATATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAG	2205
Db	2145	GAAAAATCCCCCACCATATGAAGAAGCCATGAGTGTAGCACTAAAACATCGGACTCAAAG	2204
Qy	2206	GAAGGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTAT	2265
Db	2205	GAAGAAATTAAAGAGCCTGAAAGTTTTAATGCAGCTGCTCAGGAAGCAGAAGCTCCTTAT	2264
Qy	2266	ATATCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGAT	2325
Db	2265	ATATCCATTGCATGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGAG	2324
Qy	2326	TTCTCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTA	2385
Db	2325	TTCTCTAATTATTTCAGAAATAGCAAAATTTGAGAAGTCGGTGCCTGATCACTGTGAGCTC	2384
Qy	2386	GTGGAGGATTTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCCT	2445
Db	2385	GTGGATGATTTCCTCACCCGAATCTGAACCAGTTGACTTATTTAGTGATGATTCAATTCCCT	2444
Qy	2446	GAAGTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTG	2505
Db	2445	GAAGTCCCACAAACACAAGAGGAGGCTGTGATGCTAATGAAGGAGAGTCTCACTGAAGTG	2504
Qy	2506	TCTGAGACAGTAGCCAGCACAAA---GAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
Db	2505	TCTGAGACAGTAACACAACACAAACATAAGGAGAGACTTAGTGCCTCACCTCAGGAGGTA	2564

Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCT	2622
Db	2565	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATATTACAAAAGATGCTGCATCT	2624
Qy	2623	AATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTTAAT	2682
Db	2625	AATGAAATTCCAACATTGACCAAAAAGGAGACAATTTCTTTGCAAATGGAAGAGTTTAAT	2684
Qy	2683	ACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGT	2742
Db	2685	ACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATGAAAGAAAGT	2744
Qy	2743	GAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTCTAGT	2802
Db	2745	GAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAGTTTCCACATTTGTCTAGT	2804
Qy	2803	GCTAAAGATGATTCTCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAA	2862
Db	2805	GCTAAAGATGATTCTCCT-----AAGGAGTACACTGACCTAGAAGTATCCAACAAA	2855
Qy	2863	AGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCAATTGCCTTGCTTAGAATTGCCCTGT	2922
Db	2856	AGTGAAATTGCTAATGTCCAGAGCGGGGCCAATTCGTTGCCTTGCTCAGAATTGCCCTGT	2915
Qy	2923	GACCTTTCTTTCAAGAAATATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCC	2982
Db	2916	GACCTTTCTTTCAAGAAATACATATCCTAAAGATGAAGCACATGTCTCAGATGAATTCTCC	2975
Qy	2983	GAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAA	3042
Db	2976	AAAAGTAGGTCCAGTGTATCTAAGGTGCCCTTATTGCTTCCAAATGTTTCTGCTTTGGAA	3035
Qy	3043	CCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAA	3102
Db	3036	TCTCAAATAGAAATGGGCAACATAGTTAAACCCAAAGTACTTACGAAAGAAGCAGAGGAA	3095
Qy	3103	AAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAG	3162
Db	3096	AAACTTCCTTCTGATACAGAGAAAGAGGACAGATCCCTGACAGCTGTATTGTCAGCAGAG	3155
Qy	3163	CTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTG	3222
Db	3156	CTGAATAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTG	3215
Qy	3223	GTGTTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTCAGTGTA	3282
Db	3216	GTGTTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTCAGTGTA	3275
Qy	3283	ACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGC	3342
Db	3276	ACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGT	3335
Qy	3343	GTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCATATTTAGAATCT	3402
Db	3336	GTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCATATTTGGAATCT	3395
Qy	3403	GAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTG	3462

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Db      3396 GAAGTTGCCATATCAGAGGAATTGGTTCAGAAATATAGTAATTCTGCTCTTGGTCATGTG 3455
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Qy      3523 AAGTTTGCAGTGTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACA 3582
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Db      3516 AAGTTTGCAGTGTGATGTGGGTATTTACTTACGTGGTGCCTTGTTCAATGGTTTGACA 3575
Qy      3583 CTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAG 3642
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Qy      3643 GTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAA 3702
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Db      3636 GCGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGCGTTAAGGATGCCATGGCCAAA 3695
Qy      3703 ATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
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Db      3696 ATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3733

```

#### RESULT 4

AY114152

LOCUS AY114152 3821 bp mRNA linear ROD 17-JUL-2002

DEFINITION Mus musculus nogo-A mRNA, complete cds.

ACCESSION AY114152

VERSION AY114152.1 GI:21898576

KEYWORDS .

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 3821)

AUTHORS Jin,W., Long,M., Li,R. and Ju,G.

TITLE Cloning and expression of the mouse Nogo-A protein

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 3821)

AUTHORS Jin,W., Long,M., Li,R. and Ju,G.

TITLE Direct Submission

JOURNAL Submitted (17-MAY-2002) Institute of Neurosciences, 17 Chang Le Xi  
Road, Xi'an, Shaanxi 710032, China

FEATURES Location/Qualifiers

source

1. .3821

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="BALB/c"

/db\_xref="taxon:10090"

CDS

247. .3738

/note="neurite outgrowth inhibition; RTN4; foocen"

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/protein\_id="AAM77068.1"

/db\_xref="GI:21898577"

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Db	470	CGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCG	529
Qy	542	CGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCGC	601
Db	530	CGCCCCCACC GCCCTGAGAGGCAGCCGTCCTGGGAACGCAGCCCCGCGGCGTCCGCGC	589
Qy	602	CATCCCTGCCGCCCGCTGCCGAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCTC	661
Db	590	CATCCCTGCCGCCCGCTGCCGAGTCCTGCCCTCCAAGCTCCCGAGGACGACGAGCCTC	649
Qy	662	CGGCGAGGCCCCCGCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCCGCCGCGC	721
Db	650	CAGCG-----CGGCCTCCGGCGCCAGCCGGCGCGAGCCCCCTAGCGGAGCCCCGCCGCGC	703
Qy	722	CCCCTTCCACGCCGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTTT	781
Db	704	CCCCTTCCACGCCGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTTT	763
Qy	782	TTGCTCTTCCTGCTGCATCTGAGCCTGTGATACCTCCTCTGCAGAAAAAATTATGGATT	841
Db	764	TTGCTCTTCCTGCTGCATCTGAGCCTGTGATACCTCCTCTGCAGAAAAAATTATGGATT	823
Qy	842	TGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCTCTGC	901
Db	824	TGAAGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCTCTGT	883
Qy	902	TTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAAC	961
Db	884	TTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAAC	943
Qy	962	ATGGATACCTTGGTAACTTATCAGCAGTGTATCCTCAGAAGGAACAATTGAAGAACTT	1021
Db	944	ACGGATACCTTGGTAACTTATCAGCAGTGGCATCCACAGAAGGAACATTGAAGAACTT	1003
Qy	1022	TAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGATT	1081
Db	1004	TAAATGAAGCTTCTAGAGAAATTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGAGT	1063
Qy	1082	TAGCAGAATTTTCAGAATTAGAATATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCAA	1141
Db	1064	CAGCAGAGTTTTTCAGTATTAGAATACTCAGAAATGGGATCATCTTTCAATGGCTCCCCAA	1123
Qy	1142	AAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAAG	1201
Db	1124	AAGGAGAGTCAGCCATGTTAGTAGAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAAG	1183
Qy	1202	ACAAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCT-----	1254
Db	1184	ACAAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCATAATCCACAAGAGTCACCTGCGACCC	1243
Qy	1255	-----GTGGGTAAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTTA	1306
Db	1244	TTACTAAAGTGTTAAAGAAGACGGAGTTATGTCTCCAGAAAAGACAATGGACATTTTTTA	1303

Qy	1307	ATGAAATGCAGATGTCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCAT	1366
Db	1304	ATGAAATGAAAATGTCAGTGGTAGCACCTGTGAGGGAAGAGTATGCAGATTTTAAGCCAT	1363
Qy	1367	TTGAACAAGCATGGGAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTA	1426
Db	1364	TTGAACAAGCATGGGAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTA	1423
Qy	1427	GAGCTAATGTGGAAAGTAAAGTGGACAGAAAAATGCTTGAAGATAGCCTGGAGCAAAAAA	1486
Db	1424	GAGCTAATATGGAAGTAAAGTGGACAAAAAATGCTTTGAAGATAGCCTGGAGCAAAAAA	1483
Qy	1487	GTCTTGGGAAGGATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAAGAAC	1546
Db	1484	GTCATGGGAAGGATAGTGAAGGCAGAAATGAGAATGCTTCTTTCCCCAGTACCCCAAGAAC	1543
Qy	1547	CTGTGAAGGACAGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAA	1606
Db	1544	TTGTGAAGGACGGCTCCAGAGCGTACATCACCTGTGATTCTTTACCTCAGCAACCGAGA	1603
Qy	1607	GCACCACAGCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATG	1666
Db	1604	GTACTGCAGCAAACATTTTCCCTGTGCTAGAAGATCACACTTCAGAAAATAAAACAGATG	1663
Qy	1667	AAAAAAAAATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGT	1726
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Db	1724	CAAAATCCTTTCTTGTAGCAATACATGATTCCGAGGCAGATTATGTCACAACAGATAATT	1783
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Db	1784	TATCAAAGGTGACTGAGGCAGTAGTGGCAACCATGCCTGAAGGTCTAACGCCAGATTTAG	1843
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Qy	1907	CAAAAGTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCAC	1966
Db	1904	CAAAAGTGGACTTGGTCCAGACATCAGAAGCTATACAAGAGTCAATTTACCCACAGCAC	1963
Qy	1967	AGCTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTG	2026
Db	1964	AGCTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTG	2023
Qy	2027	TTATGGAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCA	2086
Db	2024	TTATGGAAGCTCCATTAAATTCTCTCCTTCCAAGCACTGGTGCTTCTGTAGCGCAGCCCA	2083
Qy	2087	GTGTATCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTG	2146
Db	2084	GTGCATCCCCACTAGAAGTACCGTCTCCAGTTAGTTATGACGGTATAAAGCTTGAGCCTG	2143
Qy	2147	AAAACCCCCCACCATATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGG	2206

Db	2144	AAAATCCCCACCATATGAAGAAGCCATGAGTGTAGCACTAAAAACATCGGACGCAAAGG	2203
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Qy	2267	TATCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATT	2326
Db	2264	TATCCATTGCATGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGGGT	2323
Qy	2327	TCTCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAG	2386
Db	2324	TCTCTAATTATTTCAGAAATAGCAAAATTTGAGAAGTCGGTACCTGATCACTGTGAGCTCG	2383
Qy	2387	TGGAGGATTTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTG	2446
Db	2384	TGGATGATTTCCTCACCCGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTG	2443
Qy	2447	AAGTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGT	2506
Db	2444	AAGTCCCACAAACACAAGAGGAGGCTGTGATGCTAATGAAGGAGAGTCTCACTGAAGTGT	2503
Qy	2507	CTGAGACAGTAGCCCAGCACAAA---GAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAG	2563
Db	2504	CTGAGACAGTAACACAACACAATAAGGAGAGACTTAGTGCCTCACCTCAGGAGGTAG	2563
Qy	2564	GAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTA	2623
Db	2564	GAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATATTACAAAAGATGCTGCATCTA	2623
Qy	2624	ATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTTAATA	2683
Db	2624	ATGAAATTCCAACATTGACCAAAAAGGAGACAATTTCTTTGCAAATGGAAGAGTTTAATA	2683
Qy	2684	CTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTG	2743
Db	2684	CTGCAATTTATTCCAATGATGACTTACTTTCTTCTAAGGAAGACAAAATGAAAGAAAGTG	2743
Qy	2744	AAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTCAGTG	2803
Db	2744	AAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAGTTTCCACATTTGTCAGTG	2803
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Qy	2924	ACCTTTCTTTCAAGAATATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCG	2983
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KEYWORDS MGC.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 4518)  
 AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,  
 Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,  
 Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,  
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 Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,  
 Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,  
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 Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,  
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 Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.  
 TITLE Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
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 MEDLINE 22388257  
 PUBMED 12477932  
 REFERENCE 2 (bases 1 to 4518)  
 AUTHORS Strausberg,R.  
 TITLE Direct Submission  
 JOURNAL Submitted (11-AUG-2003) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
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 Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A.,  
 Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,  
 Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,  
 Casavant,T., Soares,M.B.  
 Clone distribution: MGC clone distribution information can be found  
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Db	410	 CACCGCCCCCTGAGAGGCAGCCGTCTGGGAACGCAGCCCCGCGGCGTCCGCGCCATCCCT	469
Qy	609	GCCGCCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCTCCGGCGAG	668
Db	470	 GCCGCCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCGGAGGACGACGAGCCTCCAGCG--	527
Qy	669	GCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCGCCCCCTTC	728
Db	528	 ----CGGCCTCCGGCGCCAGCCGGCGCGAGCCCCCTAGCGGAGCCCGCCGCGCCCCCTTC	583
Qy	729	CACGCCGGCCGCGCCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTTTTTGCTCT	788
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Qy	789	TCCTGCTGCATCTGAGCCTGTGATACCCTCCTCTGCAGAAAAAATTATGGATTGATGGA	848
Db	644	 TCCTGCTGCATCTGAGCCTGTGATACCCTCCTCTGCAGAAAAAATTATGGATTGAAGGA	703
Qy	849	GCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAAC	908
Db	704	 GCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGTTTGAAAC	763
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Qy	969	CCTTGGTAACTTATCAGCAGTGTCACTCCTCAGAAGGAACAATTGAAGAACTTTAAATGA	1028
Db	824	 CCTTGGTAACTTATCAGCAGTGGCATCCACAGAAGGAACATTGAAGAACTTTAAATGA	883
Qy	1029	AGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGA	1088
Db	884	 AGCTTCTAGAGAAATTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGAGTCAGCAGA	943
Qy	1089	ATTTTCAGAAATTAGAATATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGA	1148
Db	944	 GTTTTCAGTATTAGAATACTCAGAAATGGGATCATCTTTCAATGGCTCCCCAAAAGGAGA	1003
Qy	1149	GTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAAGACAAAGA	1208
Db	1004	 GTCAGCCATGTTAGTAGAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAAGACAAAGA	1063
Qy	1209	GGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCT-----	1254
Db	1064	 GGATTTAGTTTGTAGTGCAGCCCTTCATAATCCACAAGAGTCACCTGCGACCCTTACTAA	1123
Qy	1255	-GTGGGTAAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAAT	1313
Db	1124	 AGTGTTAAAGAAGACGGAGTTATGTCTCCAGAAAAGACAATGGACATTTTAAATGAAAT	1183
Qy	1314	GCAGATGTCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACA	1373



Db	1184	GAAAATGTCAGTGGTAGCACCTGTGAGGGAAGAGTATGCAGATTTTAAGCCATTGAACA	1243
Qy	1374	AGCATGGGAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAA	1433
Db	1244	AGCATGGGAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAA	1303
Qy	1434	TGTGGAAAGTAAAGTGGACAGAAAAATGCTTGGGAAGATAGCCTGGAGCAAAAAAGTCTTGG	1493
Db	1304	TATGGAAAGTAAAGTGGACAAAAATGCTTTGAAGATAGCCTGGAGCAAAAAAGGTCATGG	1363
Qy	1494	GAAGGATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAA	1553
Db	1364	GAAGGATAGTGAAGGCAGAAATGAGAATGCTTCTTTCCCCAGGACCCAGAACTTGTGAA	1423
Qy	1554	GGACAGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCAC	1613
Db	1424	GGACGGCTCCAGAGCGTACATCACCTGTGATTCTTTAGCTCAGCAACCGAGAGTACTGC	1483
Qy	1614	AGCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA	1673
Db	1484	AGCAAACATTTTCCCTGTGCTAGAAGATCACACTTCAGAAAACAAAACAGATGAAAAAAA	1543
Qy	1674	AATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCC	1733
Db	1544	AATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCC	1603
Qy	1734	TTTCCTTGTCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAA	1793
Db	1604	TTTCCTTGTCAGCAATACATGATTCTGAGGCAGATTATGTCACAACAGATAATTTATCAAA	1663
Qy	1794	GGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTTCAGGA	1853
Db	1664	GGTGACTGAGGCAGTAGTGGCAACCATGCCTGAAGGTCTAACGCCAGATTTAGTTTCAGGA	1723
Qy	1854	AGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGT	1913
Db	1724	AGCATGTGAAAGTGAAGTGAACGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGT	1783
Qy	1914	GGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTG	1973
Db	1784	GGACTTGGTCCAGACATCAGAAGCTATACAAGAGTCAATTTACCCACAGCACAGCTTTG	1843
Qy	1974	CCCATCATTTGAGGAAGCTGAAGCAACTCCGTACACAGTTTTGCCTGATATTGTTATGGA	2033
Db	1844	CCCATCATTTGAGGAAGCTGAAGCAACTCCGTACACAGTTTTGCCTGATATTGTTATGGA	1903
Qy	2034	AGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCAGTGTATC	2093
Db	1904	AGCGCCATTAAATTCTCTCCTTCCAAGCACTGGTGCTTCTGTAGCGCAGCCAGTGCATC	1963
Qy	2094	CCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCC	2153
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Qy	2274	TGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAA	2333
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Qy	2454	ACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGAC	2513
Db	2324	ACAAACACAAGAGGAGGCTGTGATGCTAATGAAGGAGAGTCTCACTGAAGTGTCTGAGAC	2383
Qy	2514	AGTAGCCCAGCACAAA---GAGGAGAGACTTAGTGCTCACCTCAGGAGCTAGGAAAAGCC	2570
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Qy	2571	ATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACAT	2630
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Qy	2811	TGATTCTCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAAT	2870
Db	2684	TGATTCTCCT-----AAGGAGTACACTGACCTAGAAGTATCCAACAAAAGTGAAAT	2734
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Db	2735	TGCTAATGTCCAGAGCGGGGCCAATTCGTTGCCTTGCTCAGAATTGCCCTGTGACCTTTC	2794
Qy	2931	TTTCAAGAATATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAG	2990
Db	2795	TTTCAAGAATACATATCCTAAAGATGAAGCACATGTCTCAGATGAATTCTCCAAAAGTAG	2854
Qy	2991	GTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGAC	3050
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Qy	3051	AGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCC	3110
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Qy	3291	CATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCA	3350
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# RESULT 6

AY102280

LOCUS AY102280 4063 bp mRNA linear ROD 29-JAN-2003

DEFINITION Mus musculus RTN4 (Rtn4) mRNA, complete cds, alternatively spliced.

ACCESSION AY102280

VERSION AY102280.1 GI:23379808

KEYWORDS .

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 4063)  
 AUTHORS Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.  
 TITLE Genomic Structure and Functional Characterisation of the Promoters  
 of Human and Mouse nogo/rtn4  
 JOURNAL J. Mol. Biol. 325 (2), 299-323 (2003)  
 MEDLINE 22376540  
 PUBMED 12488097

REFERENCE 2 (bases 1 to 4063)  
 AUTHORS Oertle,T. and Schwab,M.E.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-MAY-2002) Brain Research Institute, University of  
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REFERENCE 3 (bases 1 to 4063)  
 AUTHORS Van der Putten,H.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma  
 Inc., Basel, Switzerland

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ORIGIN

Query Match 70.9%; Score 2651; DB 10; Length 4063;  
Best Local Similarity 93.7%; Pred. No. 0;  
Matches 2804; Conservative 0; Mismatches 160; Indels 27; Gaps 3;

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Qy	888	CCCATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGT	947
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Qy	948	TTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCAGTGTCTATCCTCAGAAGGAAC	1007
Db	368	TTCTTTTAAAGAACACGGATACCTTGGTAACTTATCAGCAGTGGCATCCACAGAAGGAAC	427
Qy	1008	AATTGAAGAAACTTTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATT	1067
Db	428	TATTGAAGAAACTTTAAATGAAGCTTCTAGAGAATTGCCAGAGAGGGCAACAAATCCATT	487
Qy	1068	TGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATATTCAGAAATGGGATCATCTTT	1127
Db	488	TGTAAATAGAGAGTCAGCAGAGTTTTCAGTATTAGAATACTCAGAAATGGGATCATCTTT	547
Qy	1128	TAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAAT	1187
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Qy	1188	TGTGAGGAGTAAAGACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGA	1247
Db	608	TGTGAGGAGTAAAGACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCATAATCCACAAGA	667
Qy	1248	ATCACCT-----GTGGGTAAAGAAGACAGAGTTGTGTCTCCAGAAAAGAC	1292
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Qy	1293	AATGGACATTTTAAATGAAATGCAGATGTCAGTAGTAGCACCTGTGAGGGAAGAGTATGC	1352
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Db	908	CCTGGAGCAAAAAAGTTCATGGGAAGGATAGTGAAAGCAGAAATGAGAATGCTTCTTTCCC	967
Qy	1533	CAGTACCCCGAACCCTGTGAAGGACAGCTCCAGAGCATATATTACCTGTGCTTCCCTTAC	1592
Db	968	CAGGACCCCGAACCCTGTGAAGGACGGCTCCAGAGCGTACATCACCTGTGATTCCCTTAG	1027
Qy	1593	CTCAGCAACCGAAAGCACCACAGCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGA	1652
Db	1028	CTCAGCAACCGAGAGTACTGCAGCAAACATTTTCCCTGTGCTAGAAGATCACACTTCAGA	1087
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Db	1088	AAACAAAACAGATGAAAAAAAAATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAGAC	1147
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Qy	1773	TACAACAGATACCTTATCAAAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCT	1832
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Qy	1833	GACGCCAGATTTAGTTTCAGGAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAA	1892
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Qy	1893	GATTGCTTATGAAACAAAAGTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACT	1952
Db	1328	GATTGCTTATGAAACAAAAGTGGACTTGGTCCAGACATCAGAAGCTATACAAGAGTCAAT	1387
Qy	1953	TTACCCACAGCACAGCTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGT	2012
Db	1388	TTACCCACAGCACAGCTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGT	1447
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Db	1508	TGTAGCGCAGCCCAGTGCATCCCCACTAGAAGTACCGTCTCCAGTTAGTTATGACGGTAT	1567
Qy	2133	AAAGCTTGAGCCTGAAAACCCCCACCATATGAAGAAGCCATGAATGTAGCACTAAAAGC	2192
Db	1568	AAAGCTTGAGCCTGAAAATCCCCACCATATGAAGAAGCCATGAGTGTAGCACTAAAAC	1627
Qy	2193	TTTGGGAACAAAGGAAGGAATAAAAGAGCCTGAAAGTTTAAATGCAGCTGTTTCAGGAAAC	2252
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Qy	2253	AGAAGCTCCTTATATATCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGA	2312
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Qy	2313	GCCAAGTCCAGATTTCTCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGA	2372
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Qy	2373	ACACGCTGAGCTAGTGGAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGA	2432
Db	1808	TCACGTGAGCTCGTGGATGATTCCTCACCCGAATCTGAACCAGTTGACTTATTTAGTGA	1867
Qy	2433	TGATTCGATTCCTGAAGTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAG	2492
Db	1868	TGATTCAATTCCTGAAGTCCCACAAACACAAGAGGAGGCTGTGATGCTAATGAAGGAGAG	1927
Qy	2493	TCTCACTGAAGTGTCTGAGACAGTAGCCAGCACAAA---GAGGAGAGACTTAGTGCCTC	2549
Db	1928	TCTCACTGAAGTGTCTGAGACAGTAACACAACACAAAACATAAGGAGAGACTTAGTGCCTC	1987
Qy	2550	ACCTCAGGAGCTAGGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAA	2609
Db	1988	ACCTCAGGAGGTAGGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATATTACAAA	2047
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Qy	3090	AGAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGT	3149
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# RESULT 7

BC032272

LOCUS BC032272 3815 bp mRNA linear ROD 16-APR-2003

DEFINITION Mus musculus reticulon 4, mRNA (cDNA clone IMAGE:5366860), partial cds.

ACCESSION BC032272

VERSION BC032272.1 GI:22749634

KEYWORDS .

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 3815)

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TITLE Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 MEDLINE 22388257  
 PUBMED 12477932  
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AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: The Cepko Laboratory

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: [nisc\\_mgc@nhgri.nih.gov](mailto:nisc_mgc@nhgri.nih.gov)

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Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,

Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 65 Row: f Column: 11

This clone was selected for full length sequencing because it  
 passed the following selection criteria: Hexamer frequency ORF  
 analysis.

FEATURES Location/Qualifiers  
 source 1. .3815  
 /organism="Mus musculus"  
 /mol\_type="mRNA"



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Qy	1642	CATACTTCAGAAAATAAAACAGATGAAAAAAAAATAGAAGAAAGGAAGGCCCAAATTATA	1701	
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Qy	1702	ACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTCCCTTGTAGCAGTACAGGATTCTGAG	1761	
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Qy	3379	CCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATAC	3438
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Db	2581	AGTAATTCTGCTCTTGGTCATGTGAACAGCACAAATAAAAGAAATTGAGGCGTCTCTTCTTA	2640
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Db	2641	GTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTATTTACTTACGTT	2700
Qy	3559	GGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATT	3618
Db	2701	GGTGCCTTGTTCAATGGTTTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATT	2760
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Db	2761	CCTGTTATATATGAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAACAAG	2820
Qy	3679	AGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCA	3738
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Qy	3739	GA	3740
Db	2881	GA	2882

# RESULT 8

AB040462

LOCUS AB040462 4166 bp mRNA linear PRI 10-OCT-2001

DEFINITION Homo sapiens mRNA for RTN-xL, complete cds.

ACCESSION AB040462

VERSION AB040462.1 GI:11610574

KEYWORDS reticulon.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Tagami,S., Eguchi,Y., Kinoshita,M., Takeda,M. and Tsujimoto,Y.

TITLE A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on endoplasmic reticulum and reduces their anti-apoptotic activity

JOURNAL Oncogene 19 (50), 5736-5746 (2000)

MEDLINE 21010696

PUBMED 11126360

REFERENCE 2 (bases 1 to 4166)



Qy	139	CTCGGCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCAACAACCGCCGCGACTCTGAG	198
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Db	1021	ACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCAGAGAA	1080
Qy	1053	GGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATATTCAGA	1112
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Qy	1335	TGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAAGATAC	1394
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Qy	1503	TGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGACAGCTC	1562
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Qy	1563	CAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACACAGCAAA	1619
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Db	1738	AGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAACCCTTT	1797
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Db	1798	TCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACAAAGGT	1857
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Db	1858	GACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAGGAAGC	1917
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# ORIGIN

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Query Match      63.9%;  Score 2391.4;  DB 9;  Length 4789;
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Db 1141 AATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCAAATCC 1200

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Db 1381 TATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAAAGATA- 1439

Qy 1395 TTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTGGAAAG 1442  
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Db 1440 ---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAATCGAGAGCAACTTGAAAG 1497

Qy 1443 TAAAGTGACAGAAAATGCTTGGAGATAGCCTGGAGCAAAAAAGTCTTGGGAAGGATAG 1502  
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Db 1498 TAAAGTGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACTAATCACGAAAAAGATAG 1557

Qy 1503 TGAAGGCAGAAATGAGGATGCTTCTTTCCCAGTACCCAGAACCTGTGAAGGACAGCTC 1562  
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Db 1558 TGAGAGTAGTAATGATGATACTTCTTTCCCAGTACGCCAGAAAGGTATAAAGGATCGTTC 1617

Qy 1563 CAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACCACAGCAAAA 1619  
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Db 1618 AGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCAACAAA 1677

Qy 1620 CACTTTCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAATAGA 1679  
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Db 1678 CATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAAATAGA 1737

Qy 1680 AGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAATCCTTT 1736  
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Db 1738 AGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAACCCTTT 1797

Qy 1737 CCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGT 1796  
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Db 1798 TCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACAAAGGT 1857

Qy 1797 GACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGC 1856  
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Db 1858 GACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAGGAAGC 1917

Qy	1857	ATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGA	1916
Db	1918	ATGTGAAAGTGAATTGAATGAAGTACTGGTACAAAGATTGCTTATGAAACAAAATGGA	1977
Qy	1917	CTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTGCCC	1976
Db	1978	CTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTTTGCCC	2037
Qy	1977	ATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATGGAAGC	2036
Db	2038	ATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATGGAAGC	2097
Qy	2037	ACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGACAGCCAGTGATCCCC	2096
Db	2098	ACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCAGCTCATCACC	2157
Qy	2097	ACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCC	2156
Db	2158	ATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAACCCCCC	2214
Qy	2157	ACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAAGGAAT	2213
Db	2215	ACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAAGAAAT	2274
Qy	2214	AAAAGAGCCTGAAAGTTTAAATGCAGCTGTTCAAGAAACAGAAGCTCCTTATATATCCAT	2273
Db	2275	TAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATATCTAT	2334
Qy	2274	TGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAA	2333
Db	2335	TGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTCTCTGA	2394
Qy	2334	TTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGA	2393
Db	2395	TTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTTGAAGA	2454
Qy	2394	TTCTTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTGAAGTCCC	2453
Db	2455	TTCTTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGACGTTCC	2514
Qy	2454	ACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----AGTGTC	2507
Db	2515	ACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCATTTGA	2574
Qy	2508	TGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAA	2567
Db	2575	GTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGAGGAAA	2634
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Qy	2625	TGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTTAATAC	2684
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Db	2755	TGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAAACTGA	2814
Qy	2745	AACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTCAGTGC	2804
Db	2815	AACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCTACATTGATCAGTTC	2874
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Qy	2862	AAGTGAAATTGCTAATATCCAAAGCGGGCAGATTCAATTGCCTTGCTTAGAATTGCCCTG	2921
Db	2935	AAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCAATTGCCTTGACAGAAATTGCCCA	2994
Qy	2922	TGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCAGATGA	2975
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Qy	2976	ATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTCTCTGC	3035
Db	3055	CTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTTTCTGC	3114
Qy	3036	TTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAAGAAGC	3095
Db	3115	TTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAAGAAGC	3174
Qy	3096	AGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGAGCTGTATTGTC	3155
Db	3175	TGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATATTTTC	3234
Qy	3156	AGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGAC	3215
Db	3235	AGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGAC	3294
Qy	3216	TGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGT	3275
Db	3295	TGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTTATTGACAGTATTCAGCATTGT	3354
Qy	3276	CAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATA	3335
Db	3355	GAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATA	3414
Qy	3336	TAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTACAGGGCATATTT	3395
Db	3415	CAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTACAGGGCATATCT	3474
Qy	3396	AGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGG	3455
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Qy	3456	TCATGTGAACAGCACATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGA	3515
Db	3535	TCATGTGAACAGCACATAAAGGAACTGAGGCGCCTCTTCTTAGTTGATGATTTAGTTGA	3594
Qy	3516	TTCCCTGAAGTTTGAGTGTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGG	3575



Db 3595 TTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGG 3654  
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 Db 3715 GCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTAT 3774  
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# RESULT 10

AC131431/c

LOCUS AC131431 218532 bp DNA linear HTG 19-NOV-2002

DEFINITION Rattus norvegicus clone CH230-256K14, WORKING DRAFT SEQUENCE.

ACCESSION AC131431

VERSION AC131431.3 GI:25084347

KEYWORDS HTG; HTGS\_PHASE2; HTGS\_DRAFT; HTGS\_FULLLTOP.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1 (bases 1 to 218532)

AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,  
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,  
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Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,  
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Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,  
Weinstock,G. and Gibbs,R.A.

TITLE Direct Submission  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 218532)  
AUTHORS Rat Genome Sequencing Consortium.  
TITLE Direct Submission  
JOURNAL Submitted (22-AUG-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
REFERENCE 3 (bases 1 to 218532)  
AUTHORS Rat Genome Sequencing Consortium.  
TITLE Direct Submission  
JOURNAL Submitted (19-NOV-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
COMMENT On Nov 19, 2002 this sequence version replaced gi:23101715.  
The sequence in this assembly is a combination of BAC based reads  
and whole genome shotgun sequencing reads assembled using Atlas  
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described  
in the feature table below represents a scaffold in the Atlas  
assembly (a 'contig-scaffold'). Within each contig-scaffold,  
individual sequence contigs are ordered and oriented, and separated  
by sized gaps filled with Ns to the estimated size. The sequence  
may extend beyond the ends of the clone and there may be sequence  
contigs within a contig-scaffold that consist entirely of whole  
genome shotgun sequence reads. Both end sequences and whole genome  
shotgun sequence only contigs will be indicated in the feature  
table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
----- Project Information  
Center project name: GMSN  
Center clone name: CH230-256K14  
----- Summary Statistics

Assembly program: Phrap; version 0.990329  
Consensus quality: 185268 bases at least Q40  
Consensus quality: 186898 bases at least Q30  
Consensus quality: 188068 bases at least Q20  
Estimated insert size: 191844; sum-of-contigs estimation  
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

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\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 1 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submittor.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
\* 1 218532: contig of 218532 bp in length.

FEATURES  
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    misc\_feature 1. .2141  
        /note="wgs\_contig"

ORIGIN

Query Match                   62.9%;   Score 2353.8;   DB 2;   Length 218532;  
Best Local Similarity   99.7%;   Pred. No. 0;  
Matches 2358;   Conservative   0;   Mismatches   7;   Indels   0;   Gaps   0;

Qy           824 CAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGG 883  
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Db   147688 CAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGG  
147629  
  
Qy           884 ATTTCCCATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAA 943  
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Db   147628 ATTTCCCATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAA  
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Db   147568 CTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCAGTGTTCATCCTCAGAAG  
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Qy           1064 CATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATATTCAGAAATGGGATCAT 1123  
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Db	146308		AGGAAGGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTT	
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	146129			
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RESULT 11  
 AC133315

LOCUS AC133315 238341 bp DNA linear HTG 19-NOV-2002  
 DEFINITION Rattus norvegicus clone CH230-525J22, WORKING DRAFT SEQUENCE, 2  
 unordered pieces.

ACCESSION AC133315

VERSION AC133315.2 GI:25073594

KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE 1 (bases 1 to 238341)

AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,  
 Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,  
 Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,  
 Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,  
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 Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,  
 Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,  
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 Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,  
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TITLE Direct Submission  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 238341)  
AUTHORS Rat Genome Sequencing Consortium.  
TITLE Direct Submission  
JOURNAL Submitted (10-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
REFERENCE 3 (bases 1 to 238341)  
AUTHORS Rat Genome Sequencing Consortium.  
TITLE Direct Submission  
JOURNAL Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
COMMENT On Nov 19, 2002 this sequence version replaced gi:22771260. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
----- Project Information  
Center project name: KAYT  
Center clone name: CH230-525J22  
----- Summary Statistics  
Assembly program: Phrap; version 0.990329  
Consensus quality: 219617 bases at least Q40  
Consensus quality: 221191 bases at least Q30  
Consensus quality: 222226 bases at least Q20  
Estimated insert size: 224889; sum-of-contigs estimation  
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation  
-----

\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).



\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 2 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

\* 1 237118: contig of 237118 bp in length  
 \* 237119 237218: gap of unknown length  
 \* 237219 238341: contig of 1123 bp in length.

FEATURES Location/Qualifiers  
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 /db\_xref="taxon:10116"  
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 site:  
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#### ORIGIN

Query Match 62.9%; Score 2353.8; DB 2; Length 238341;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 2358; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 824 CAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGG 883  
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 Db 126178 CAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGG  
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 Qy 884 ATTTCCCATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAA 943  
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 Db 126238 ATTTCCCATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAA  
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 Qy 944 CTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCAGTGTCTCCTCAGAAG 1003  
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 Db 126298 CTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCAGTGTCTCCTCAGAAG  
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 Db 126358 GAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATC  
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RESULT 12

AX195249

LOCUS AX195249 4053 bp RNA linear PAT 28-AUG-2001

DEFINITION Sequence 5 from Patent WO0151520.

ACCESSION AX195249

VERSION AX195249.1 GI:15385809

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Strittmatter, S.M.

TITLE Nogo receptor-mediated blockade of axonal growth

JOURNAL Patent: WO 0151520-A 5 19-JUL-2001;

YALE UNIVERSITY (US)

FEATURES Location/Qualifiers

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/db\_xref="taxon:9606"

CDS 135. .3713

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LPHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPDVSALATQAEIESIVKPKV  
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QKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFVLMVWVFTYVGALFNGLTLLILALI  
SLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE"

ORIGIN

Query Match 62.6%; Score 2343.6; DB 6; Length 4053;  
Best Local Similarity 81.3%; Pred. No. 0;  
Matches 3017; Conservative 0; Mismatches 574; Indels 119; Gaps 21;

Qy		CACGACTCGGCCTGCCTGGCCCTGCCAGTCTTGCCCCAACCCCACAACC GCCC GCGACT	193
Db	16	CTCGGCTCAGTCGGCCCAGCCCTCTCAGTCCTCCCAACCCCACAACC GCCC GC GGCT	75
Qy	194	CTGAGGAGAAGCGGC-CCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCC	252
Db	76	CTGAGACGCGGCCCCGGCGGCGGCGGCAGCAGCTGCAGCATCATC-TCCACCCTCCAGCC	134
Qy	253	ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCGCCCGGCCT	312
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Qy	313	CCGCCCCGCTTCAAGTACCAGTTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG	372
Db	192	CAGCCCGCGTTC AAGTACCAGTTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG	248
Qy	373	GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGA ACTGGAGGTGCTGGAGAGGAAG	432
Db	249	GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG	308
Qy	433	CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCGCCGCCGCCGCGCCGCTG	486
Db	309	CCCGCCGCCGGGCTGTCCGCGGCC CAGTGCCACCGCCCC TGCCCGGCGCGCCCCCTG	368
Qy	487	CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCC	546
Db	369	ATGGACTTCGAAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC	428
Qy	547	CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC	597
Db	429	CCCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTCGACCGTGCCC	488
Qy	598	GCGCCATCCCTGCCGCCCGCTGCCGCAGT CCTGCCCTCCAAGCT CCCAGAGGACGACGAG	657
Db	489	GCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG	548
Qy	658	CCTCCGGCGAGGCCCGCCCTCCGCCGCCAGCCGGCGGAGCCCCCTGGCGGAG-----	711
Db	549	CCTCCGGCCCCGGCCTCCCCCTCCTCCCCGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG	608
Qy	712	-----CCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC	750
Db	609	TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCCGCCGCGCCCAAGCGC	668
Qy	751	AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT	807
Db	669	AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT	728
Qy	808	GTGATA CCCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT	867
Db	729	GTGATACGCTCCTCTGCAGAAA--TATGGACTTGAAGGAGCAGCCAGGTAACACTATT	785
Qy	868	TCGTCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAAACTGCTGCCTCTCTTCCTTCT	927

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      ||| |||||
Db      786 TCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCTTCTCTTCTCTTCT 845
Qy      928 CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA 987
      || |||||
Db      846 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAGAACATGAATACCTTGGTAATTTGTCAACA 905
Qy      988 GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA 1047
      || ||| ||| ||||| || ||||| || ||||| ||||| || ||
Db      906 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 965
Qy     1048 GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT 1107
      |||| |||| || || || || ||||| |||| ||||| |||||
Db     966 GAGAAGGCAAAAACCTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC 1025
Qy     1108 TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA 1167
      ||||| ||||| || || || ||||| || || || || ||||| ||
Db     1026 TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 1085
Qy     1168 AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT 1224
      || ||| ||||| |||| |||| || |||| || ||||| || ||
Db     1086 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1145
Qy     1225 GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC 1269
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Db     1146 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1205
Qy     1270 AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA 1329
      ||||| ||||| |||| |||| ||||| ||||| || ||||| ||
Db     1206 GAAGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTGGA 1265
Qy     1330 GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA 1389
      || ||| ||||| || ||||| || ||||| || ||||| |||||
Db     1266 GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA 1325
Qy     1390 GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG 1437
      |||| || |||| || |||| |||| ||||| ||||| || ||
Db     1326 GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG 1382
Qy     1438 GAAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGGAAG 1497
      ||||| ||||| || ||||| || ||||| ||||| || || ||
Db     1383 GAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAAAAA 1442
Qy     1498 GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC 1557
      ||||| || || ||||| || ||||| ||||| ||||| || |||||
Db     1443 GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT 1502
Qy     1558 AGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACCACA 1614
      || || ||||| || ||||| ||||| || ||||| || |||||
Db     1503 CGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA 1562
Qy     1615 GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA 1674
      ||||| || ||||| |||| ||||| || ||||| |||||
Db     1563 ACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAA 1622
Qy     1675 ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT 1731
      ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db	1623	ATAGAAGAAAAGAAGGCCCAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAAC	1682
Qy	1732	CCTTTCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Db	1683	CCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA	1742
Qy	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG	1851
Db	1743	AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG	1802
Qy	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Db	1803	GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA	1862
Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATAACAAGAATCACTTTACCCACAGCACAGCTT	1971
Db	1863	ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT	1922
Qy	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	2031
Db	1923	TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG	1982
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA	2091
Db	1983	GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTCGATACAGCCCAGCTCA	2042
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Db	2043	TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAACATGAGCCTGAAAAC	2099
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
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Qy	2209	GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268
Db	2160	GAAATTAAAGAGCCTGAAAAATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA	2219
Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTC	2328
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Qy	2329	TCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
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Qy	2389	GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCTTGAA	2448
Db	2340	GAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2399
Qy	2449	GTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2400	GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2459
Qy	2503	GTGTCTGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
Db	2460	TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAAAGTCAAGTCTTGGCCACCTGAGGGA	2519



Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
Db	2520	GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA	2579
Qy	2620	TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTT	2679
Db	2580	CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTC	2639
Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA	2739
Db	2640	AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2699
Qy	2740	AGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCCACGTTTGTC	2799
Db	2700	ACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCTTACATTGATC	2759
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Qy	2857	GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTTCATTGCCTTGCTTAGAATTG	2916
Db	2820	CACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTTCATTGCCTTGACACAGAATTG	2879
Qy	2917	CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA	2970
Db	2880	CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA	2939
Qy	2971	GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC	3030
Db	2940	GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT	2999
Qy	3031	TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA	3090
Db	3000	TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA	3059
Qy	3091	GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAAGAGGACAGATCCCTGTCAGCTGTA	3150
Db	3060	GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	3119
Qy	3151	TTGTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG	3210
Db	3120	TTTTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG	3179
Qy	3211	AAGACTGGAGTGGTGTTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGC	3270
Db	3180	AAGACTGGAGTGGTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGC	3239
Qy	3271	ATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG	3330
Db	3240	ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG	3299
Qy	3331	ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA	3390
Db	3300	ATATACAAGGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA	3359

Qy 3391 TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT 3450  
 ||| | ||||||||||||||||||| |||| | |||||||||||||||  
 Db 3360 TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT 3419  
 Qy 3451 CTTGGTCATGTGAACAGCACAAATAAAGAAGCTGAGGCGGCTTTTCTTAGTTGATGATTTA 3510  
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 Db 3420 CTTGGTCATGTGAAGTGCACGATAAAGGAAGCTCAGGCGCCTCTTCTTAGTTGATGATTTA 3479  
 Qy 3511 GTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT 3570  
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 Db 3480 GTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT 3539  
 Qy 3571 AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT 3630  
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 Db 3540 AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT 3599  
 Qy 3631 GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT 3690  
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 Db 3600 GAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT 3659  
 Qy 3691 GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740  
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 Db 3660 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3709

# RESULT 13

AB020693

LOCUS AB020693 4053 bp mRNA linear PRI 16-JUN-1999

DEFINITION Homo sapiens mRNA for KIAA0886 protein, complete cds.

ACCESSION AB020693

VERSION AB020693.1 GI:4240260

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (sites)

AUTHORS Nagase,T., Ishikawa,K., Suyama,M., Kikuno,R., Hirose,M.,  
 Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.

TITLE Prediction of the coding sequences of unidentified human genes.  
 XII. The complete sequences of 100 new cDNA clones from brain which  
 code for large proteins in vitro

JOURNAL DNA Res. 5 (6), 355-364 (1998)

MEDLINE 99156230

PUBMED 10048485

REFERENCE 2 (bases 1 to 4053)

AUTHORS Ohara,O., Suyama,M., Kikuno,R., Nagase,T. and Ishikawa,K.

TITLE Direct Submission

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 Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba  
 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,  
 Fax:+81-438-52-3914)

FEATURES

source Location/Qualifiers  
 1. .4053  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"



Accession	Position	Sequence	Length
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Qy	433	CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCCGCCGCCGCCGCCGCTG	486
Db	309	CCCGCCGCCGGGCTGTCCGCGGCCCCAGTGCCACCGCCCCCTGCCGCCGGCGCGCCCTG	368
Qy	487	CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCC	546
Db	369	ATGGACTTCGGAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC	428
Qy	547	CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC	597
Db	429	CCCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTGACCGTGCCC	488
Qy	598	GCGCCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCAGAGGACGACGAG	657
Db	489	GCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG	548
Qy	658	CCTCCGGCGAGGCCCCCGCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG-----	711
Db	549	CCTCCGGCCCCGGCCTCCCCCTCCTCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG	608
Qy	712	-----CCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC	750
Db	609	TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCGCGCCGCGCCCAAGCGC	668
Qy	751	AGGGGCTCC---GGCTCAGTGGATGAGACCCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT	807
Db	669	AGGGGCTCCTCGGGCTCAGTGGATGAGACCCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT	728
Qy	808	GTGATACCCCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT	867
Db	729	GTGATACGCTCCTCTGCAGAAA--TATGGACTTGAAGGAGCAGCCAGGTAACACTATT	785
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Db	846	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	905
Qy	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
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Db	966	GAGAAGGCAAAAACCTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC	1025
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Db	1206	GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGA	1265
Qy	1330	GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA	1389
Db	1266	GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA	1325
Qy	1390	GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG	1437
Db	1326	GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG	1382
Qy	1438	GAAAGTAAAGTGGACAGAAAATGCTTGGAGATAGCCTGGAGCAAAAAAGTCTTGGGAAG	1497
Db	1383	GAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACTAATCACGAAAAA	1442
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Qy	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT	1731
Db	1623	ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAAC	1682
Qy	1732	CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
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Qy	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG	1851
Db	1743	AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG	1802
Qy	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Db	1803	GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA	1862
Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
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Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA	2091
Db	1983	GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA	2042
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Db	2043	TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	2099
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	2100	CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAAGTATCAGGAATAAAGGAA	2159
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Db	2160	GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTCAAGGAAACAGAAGCTCCTTATATA	2219
Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC	2328
Db	2220	TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTTC	2279
Qy	2329	TCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Db	2280	TCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2339
Qy	2389	GAGGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTGAA	2448
Db	2340	GAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2399
Qy	2449	GTCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2400	GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2459
Qy	2503	GTGTCTGAGACAGTAGCCACGACAAAGAGGAGAGACTTAGTGCCCTCACCTCAGGAGCTA	2562
Db	2460	TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA	2519
Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
Db	2520	GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA	2579
Qy	2620	TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTT	2679
Db	2580	CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAGCTC	2639
Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAGAA	2739
Db	2640	AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2699
Qy	2740	AGTGAAACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC	2799
Db	2700	ACTGAAACGTTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTTCCTACATTGATC	2759
Qy	2800	AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC	2856
Db	2760	AGTTCTAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC	2819

Qy	2857	GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTG	2916
Db	2820	CACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCATTGCCTTGACAGAATTG	2879
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Qy	2971	GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC	3030
Db	2940	GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT	2999
Qy	3031	TCTGCTTTGGAACCTCAGACAGAAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA	3090
Db	3000	TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA	3059
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Db	3060	GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	3119
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Qy	3211	AAGACTGGAGTGGTGTTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGC	3270
Db	3180	AAGACTGGAGTGGTGTTTGGTGCCAGCTTATTCCTGCTGCTTTTATTGACAGTATTCAGC	3239
Qy	3271	ATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG	3330
Db	3240	ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG	3299
Qy	3331	ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCA	3390
Db	3300	ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCA	3359
Qy	3391	TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTTCAGAAATACAGTAATTCTGCT	3450
Db	3360	TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGTAATTCTGCT	3419
Qy	3451	CTTGGTTCATGTGAACAGCACAAATAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA	3510
Db	3420	CTTGGTTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA	3479
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Db	3480	GTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT	3539
Qy	3571	AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT	3630
Db	3540	AATGGTCTGACACTACTGATTTTGGCTCTCATTCACTCTTCAGTGTTTCTGTTATTTAT	3599
Qy	3631	GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT	3690
Db	3600	GAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAGAT	3659
Qy	3691	GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA	3740

Db 3660 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3709

RESULT 14

AF148537

LOCUS AF148537 4632 bp mRNA linear PRI 09-SEP-2000

DEFINITION Homo sapiens reticulon 4a mRNA, complete cds.

ACCESSION AF148537

VERSION AF148537.1 GI:10039550

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4632)

AUTHORS Yang, J., Yu, L., Bi, A.D. and Zhao, S.Y.

TITLE Assignment of the human reticulon 4 gene (RTN4) to chromosome  
2p14-->2p13 by radiation hybrid mapping

JOURNAL Cytogenet. Cell Genet. 88 (1-2), 101-102 (2000)

MEDLINE 20237542

PUBMED 10773680

REFERENCE 2 (bases 1 to 4632)

AUTHORS Zhou, Y., Yu, L. and Zhao, S.Y.

TITLE Direct Submission

JOURNAL Submitted (05-MAY-1999) Lab of Human Gene Research, Institute of  
Genetics, Fudan University, No. 220 Handan Rd., Shanghai 200433,  
P.R.China

FEATURES Location/Qualifiers

source

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CDS

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polyA_signal
polyA_site
ORIGIN

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Db	23	CTCGGCTCAGTCGGCCCAGCCCCTCTCAGTCCTCCCCAACCCCCACAACCGCCCGCGGCT	82
Qy	194	CTGAGGAGAAGCGGC-CCTGCGGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCC	252
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Qy	373	GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG	432
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Qy	433	CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCGCCGCCGCCGCGCCGCTG	486
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Qy	487	CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCC	546
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Qy	547	CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC	597
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Db	496	GCGCCATCCCCGCTGTCTGCTGCCGCGAGTCTGCCCTCCAAGCTCCCTGAGGACGACGAG	555
Qy	658	CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGGAGCCCCCTGGCGGAG-----	711
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Qy	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
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Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
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Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
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Qy	1168	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT	1224
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Qy	1270	AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA	1329
Db	1213	GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGA	1272
Qy	1330	GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA	1389
Db	1273	GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA	1332
Qy	1390	GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG	1437
Db	1333	GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG	1389
Qy	1438	GAAAGTAAAGTGGACAGAAAATGCTTGAAGATAGCCTGGAGCAAAAAAGTCTTGGGAAG	1497
Db	1390	GAAAGTAAAGTGGATAAAAAATGTTTGCAGATAGCCTTGAGCAAACTAATCACGAAAA	1449
Qy	1498	GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC	1557
Db	1450	GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT	1509
Qy	1558	AGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACCACA	1614
Db	1510	CGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATTGCA	1569

Qy	1615	GCAAACACTTTCCCTTTGTTAGGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA	1674
Db	1570	ACAAACATTTTTCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAA	1629
Qy	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT	1731
Db	1630	ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAAC	1689
Qy	1732	CCTTTCTTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
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Qy	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTTCAG	1851
Db	1750	AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG	1809
Qy	1852	GAAGCATGTGAAAGTGAACCTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Db	1810	GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA	1869
Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Db	1870	ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT	1929
Qy	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	2031
Db	1930	TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG	1989
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGACGCCAGTGTA	2091
Db	1990	GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA	2049
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Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC	2328
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Qy	2329	TCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
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Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
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Db	2587	CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAGCTC	2646
Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA	2739
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Db	3067	GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	3126
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[illegible]

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Qy	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT	1731
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Db	1699	 CCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA	1758
Qy	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG	1851
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Qy	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Db	1819	 GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA	1878
Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Db	1879	 ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT	1938
Qy	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	2031
Db	1939	 TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG	1998
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCAGTGTA	2091
Db	1999	 GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCAGCTCA	2058
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Db	2059	 TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	2115
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	2116	 CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA	2175
Qy	2209	GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268
Db	2176	 GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA	2235
Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTT	2328



Db	2236	TCTATTGCATGTGATTTAATTAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTC	2295
Qy	2329	TCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Db	2296	TCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2355
Qy	2389	GAGGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCCTGAA	2448
Db	2356	GAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2415
Qy	2449	GTCCCAACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2416	GTTCACAAAAACAAGATGAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2475
Qy	2503	GTGTCTGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
Db	2476	TTTGAGTCAATGATAGAATATGAAAAATAAGGAAAAAAGTCTAGTGCCTTGCCACCTGAGGGA	2535
Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
Db	2536	GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA	2595
Qy	2620	TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTT	2679
Db	2596	CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTC	2655
Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA	2739
Db	2656	AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2715
Qy	2740	AGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC	2799
Db	2716	ACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCTACATTGATC	2775
Qy	2800	AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC	2856
Db	2776	AGTTCTAAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC	2835
Qy	2857	GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTG	2916
Db	2836	CACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCTATTGCCTTGACAGAAATTG	2895
Qy	2917	CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA	2970
Db	2896	CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA	2955
Qy	2971	GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC	3030
Db	2956	GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT	3015
Qy	3031	TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA	3090
Db	3016	TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA	3075
Qy	3091	GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA	3150
Db	3076	GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	3135

Qy 3151 TTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG 3210  
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 Db 3136 TTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG 3195  
 Qy 3211 AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGC 3270  
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 Db 3196 AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGC 3255  
 Qy 3271 ATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG 3330  
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 Db 3256 ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG 3315  
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 Db 3316 ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA 3375  
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 Db 3376 TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT 3435  
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 Db 3436 CTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA 3495  
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 Qy 3571 AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT 3630  
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 Db 3556 AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTTCTGTTATTTAT 3615  
 Qy 3631 GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT 3690  
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 Db 3616 GAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT 3675  
 Qy 3691 GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740  
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 Db 3676 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3725

Search completed: September 11, 2004, 10:10:10  
 Job time : 14092.4 secs

OM nucleic - nucleic search, using sw model

Run on: September 10, 2004, 23:36:15 ; Search time 1309.89 Seconds  
(without alignments)  
12132.674 Million cell updates/sec

Title: US-09-830-972-1  
Perfect score: 3741  
Sequence: 1 attgctcgtctctgggcggcgg.....gattgaagcgcaaagcagat 3741

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002s:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3739.4	100.0	4684	3	AAD01173	Aad01173 Rat neuri
2	3739.4	100.0	4684	6	ABN86600	Abn86600 Rat neuro
3	2343.6	62.6	4053	4	AAS09453	Aas09453 Human cDN
4	2343.6	62.6	4053	8	ACC81048	Acc81048 Human Nog
5	2343.6	62.6	4632	6	ABV94680	Abv94680 Human pan
6	2333.2	62.4	4093	3	AAA23454	Aaa23454 cDNA enco
7	2323.8	62.1	4822	6	ABS70449	Abs70449 Human bon

	8	2297.4	61.4	4698	7	ABX34563	Abx34563	Human mdd
	9	2289.2	61.2	3579	3	AAZ56886	Aaz56886	Human MAG
	10	2289.2	61.2	3579	4	AAF90324	Aaf90324	Human NOG
	11	2289.2	61.2	3579	6	ABK90134	Abk90134	DNA encod
	12	2289.2	61.2	3579	6	ABN86601	Abn86601	Human neu
	13	1869.8	50.0	3833	3	AAD01174	Aad01174	Bovine ne
	14	1411.2	37.7	2386	2	AAV30920	Aav30920	Human sec
	15	1408	37.6	2386	5	AAF98399	Aaf98399	Human cDN
	16	1088.8	29.1	1980	4	AAI98079	Aai98079	Human neu
	17	809.8	21.6	2782	9	ADB85284	Adb85284	Rat fooce
	18	564	15.1	1568	3	AAD01175	Aad01175	Rat neur
c	19	503.2	13.5	1758	4	AAF32725	Aaf32725	Human sec
	20	498	13.3	2100	7	ABT42936	Abt42936	Human neu
	21	497.4	13.3	600	4	AAF90323	Aaf90323	Human NOG
	22	497.4	13.3	770	3	AAA72983	Aaa72983	Human NSP
	23	497.4	13.3	799	2	AAV23695	Aav23695	Human NSP
	24	497.4	13.3	1122	3	AAZ56888	Aaz56888	Human MAG
	25	497.4	13.3	1122	4	AAF90325	Aaf90325	Human NOG
	26	497.4	13.3	1213	2	AAX04379	Aax04379	Human sec
	27	497.4	13.3	1216	6	ABA05903	Aba05903	Human RTN
	28	497.4	13.3	2052	6	ABK90133	Abk90133	DNA encod
	29	497.4	13.3	2235	6	ABV94681	Abv94681	Human pan
	30	497.4	13.3	2240	3	AAC64406	Aac64406	Human Nog
	31	495.8	13.3	991	2	AAX97587	Aax97587	Extended
	32	495.8	13.3	1610	3	AAZ36230	Aaz36230	cDNA enco
	33	495.8	13.3	1694	4	AAK94408	Aak94408	Human ful
	34	483.6	12.9	868	3	AAZ56887	Aaz56887	Human MAG
	35	475	12.7	1798	6	ABK90135	Abk90135	DNA encod
	36	468	12.5	1514	6	ABK34580	Abk34580	Human cDN
	37	391.6	10.5	1683	4	AAD08386	Aad08386	Human sec
	38	375.6	10.0	422	7	ABX43312	Abx43312	Bovine ES
	39	374	10.0	422	7	ABX46402	Abx46402	Bovine ES
	40	323	8.6	460	2	AAV87027	Aav87027	EST clone
	41	322.4	8.6	389	7	ABX39989	Abx39989	Bovine ES
	42	316.2	8.5	615	4	AAK93939	Aak93939	Human cDN
	43	302.6	8.1	423	7	ABX43927	Abx43927	Bovine ES
	44	299	8.0	562	4	AAK93574	Aak93574	Human cDN
c	45	278.8	7.5	742	4	AAI96236	Aai96236	Human neu

#### ALIGNMENTS

##### RESULT 1

AAD01173

ID AAD01173 standard; cDNA; 4684 BP.

XX

AC AAD01173;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat neurite growth inhibitor Nogo A cDNA.

XX

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;  
KW central nervous system; neoplastic disease; antiproliferative; glioma;  
KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;  
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;

KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
 KW structural plasticity; screening; ss.  
 XX  
 OS Rattus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 253. .3744  
 FT /\*tag= a  
 FT /product= "Nogo A"  
 FT /transl\_except= (pos:1462. .1464, aa:Ile)  
 XX  
 PN WO200031235-A2.  
 XX  
 PD 02-JUN-2000.  
 XX  
 PF 05-NOV-1999; 99WO-US026160.  
 XX  
 PR 06-NOV-1998; 98US-0107446P.  
 XX  
 PA (SCHW/) SCHWAB M E.  
 PA (CHEN/) CHEN M S.  
 XX  
 PI Schwab ME, Chen MS;  
 XX  
 DR WPI; 2000-400052/34.  
 DR P-PSDB; AAY71310.  
 XX  
 PT Nogo proteins and nucleic acids useful for treating neoplastic disorders  
 PT of the central nervous system and inducing regeneration of neurons.  
 XX  
 PS Claim 26; Fig 2A; 122pp; English.  
 XX  
 CC The present sequence is a cDNA encoding rat Nogo A protein which is a  
 CC potent neural cell growth inhibitor and is free of all central nervous  
 CC system (CNS) myelin material with which it is natively associated. The  
 CC present sequence was generated by fusing R018U37-3, R1-3U21 cDNA  
 CC sequences isolated from hexanucleotides-primed rat brain stem/spinal cord  
 CC library, and Olil8 cDNA from an oligo d(T)-primed rat oligodendrocyte  
 CC library. Nogo proteins and fragments displaying neurite growth inhibitory  
 CC activity are used in the treatment of neoplastic disease of the CNS e.g.  
 CC glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma,  
 CC pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma,  
 CC menagioma, neuroblastoma or retinoblastoma and degenerative nerve  
 CC diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which  
 CC promote Nogo activity can be used to treat or prevent hyperproliferative  
 CC or benign dysproliferative disorders e.g. psoriasis and tissue  
 CC hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to  
 CC inhibit production of Nogo protein to induce regeneration of neurons or  
 CC to promote structural plasticity of the CNS in disorders where neurite  
 CC growth, regeneration or maintenance are deficient or desired. The animal  
 CC models can be used in diagnostic and screening methods for predisposition  
 CC to disorders and to screen for or test molecules which can treat or  
 CC prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are  
 CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the  
 CC specification. However the specification does not include sequences for  
 CC these SEQ ID numbers

XX

SQ Sequence 4684 BP; 1358 A; 1048 C; 1112 G; 1166 T; 0 U; 0 Other;

Query Match 100.0%; Score 3739.4; DB 3; Length 4684;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3740; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 ATTGCTCGTCTGGGCGGCGGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCG 60
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Db      1 ATTGCTCGTCTGGGCGGCGGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCG 60

Qy     61 ATCGCGAAGGCAGCAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTCTT 120
      ||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db     61 ATCGCGAAGGCAGGAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTCTT 120

Qy    121 CGGCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACA 180
      ||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    121 CGGCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACA 180

Qy    181 ACCGCCCCGCGACTCTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGC 240
      ||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    181 ACCGCCCCGCGACTCTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGC 240

Qy    241 GACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGC 300
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Db    241 GACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGC 300

Qy    301 CCGCCCCGGCCTCCGCCCCGCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAG 360
      ||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    301 CCGCCCCGGCCTCCGCCCCGCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAG 360

Qy    361 GACGAGGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTG 420
      ||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    361 GACGAGGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTG 420

Qy    421 CTGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCGCCGCG 480
      ||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    421 CTGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCGCCGCG 480

Qy    481 CCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCC 540
      ||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    481 CCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCC 540

Qy    541 GCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCG 600
      ||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    541 GCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCG 600

Qy    601 CCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCT 660
      ||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    601 CCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCT 660

Qy    661 CCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCG 720
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Db    661 CCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCG 720

Qy    721 CCCCCTTCCACGCCGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTT 780
      ||||||||||| ||||||||||||||||||||||||||||||||||||||||
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Db	721	CCCCCTTCCACGCCGCGCCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTT	780
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Db	781	TTTGCTCTTCCTGCTGCATCTGAGCCTGTGATACCCTCCTCTGCAGAAAAAATTATGGAT	840
Qy	841	TTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTG	900
Db	841	TTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTG	900
Qy	901	CTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAA	960
Db	901	CTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAA	960
Qy	961	CATGGATACCTTGGTAACTTATCAGCAGTGTCTCCTCAGAAGGAACAATTGAAGAACT	1020
Db	961	CATGGATACCTTGGTAACTTATCAGCAGTGTCTCCTCAGAAGGAACAATTGAAGAACT	1020
Qy	1021	TTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGAT	1080
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Db	1081	TTAGCAGAATTTTCAGAATTAGAATATTAGAAATGGGATCATCTTTTAAAGGCTCCCCA	1140
Qy	1141	AAAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA	1200
Db	1141	AAAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA	1200
Qy	1201	GACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCTGTGGGT	1260
Db	1201	GACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCTGTGGGT	1260
Qy	1261	AAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTTAATGAAATGCAGATG	1320
Db	1261	AAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTTAATGAAATGCAGATG	1320
Qy	1321	TCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGG	1380
Db	1321	TCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGG	1380
Qy	1381	GAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTGGAA	1440
Db	1381	GAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTGGAA	1440
Qy	1441	AGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAGTCTTGGAAGGAT	1500
Db	1441	AGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAGTCTTGGAAGGAT	1500
Qy	1501	AGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGACAGC	1560
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Qy	1621	ACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAAATAAAACAGATGAAAAAAAAATAGAA	1680
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Qy	1681	GAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTCCTT	1740
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Qy	1801	GAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGCATGT	1860
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Qy	1861	GAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTG	1920
Db	1861	GAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTG	1920
Qy	1921	GTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTGCCCATCA	1980
Db	1921	GTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTGCCCATCA	1980
Qy	1981	TTTGAGGAAGCTGAAGCAACTCCGTCAACAGTTTTGCCTGATATTGTTATGGAAGCACCA	2040
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Qy	2041	TTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCACTG	2100
Db	2041	TTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCACTG	2100
Qy	2101	GAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCACCA	2160
Db	2101	GAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCACCA	2160
Qy	2161	TATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAG	2220
Db	2161	TATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAG	2220
Qy	2221	CCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGT	2280
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Qy	2281	GATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTCA	2340
Db	2281	GATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTCA	2340
Qy	2341	GAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCTCTCA	2400
Db	2341	GAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCTCTCA	2400
Qy	2401	CCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTGAAGTCCCACAAACA	2460
Db	2401	CCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTGAAGTCCCACAAACA	2460



Qy	2461	CAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCC	2520
Db	2461	CAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCC	2520
Qy	2521	CAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAGCCATATTTAGAG	2580
Db	2521	CAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAGCCATATTTAGAG	2580
Qy	2581	TCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTG	2640
Db	2581	TCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTG	2640
Qy	2641	ACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAAT	2700
Db	2641	ACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAAT	2700
Qy	2701	GATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCA	2760
Db	2701	GATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCA	2760
Qy	2761	TCTCCGATTGAGATAATAGATGAATTTCCCACGTTTGTGCTGCTAAAGATGATTCTCCT	2820
Db	2761	TCTCCGATTGAGATAATAGATGAATTTCCCACGTTTGTGCTGCTAAAGATGATTCTCCT	2820
Qy	2821	AAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATC	2880
Db	2821	AAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATC	2880
Qy	2881	CAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAAT	2940
Db	2881	CAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAAT	2940
Qy	2941	ATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTA	3000
Db	2941	ATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTA	3000
Qy	3001	TCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGC	3060
Db	3001	TCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGC	3060
Qy	3061	AGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACA	3120
Db	3061	AGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACA	3120
Qy	3121	GAGAAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACCTTCAGTT	3180
Db	3121	GAGAAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACCTTCAGTT	3180
Qy	3181	GTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTA	3240
Db	3181	GTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTA	3240
Qy	3241	TTCTGCTGCTGTCTCTGACAGTGTTTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTG	3300
Db	3241	TTCTGCTGCTGTCTCTGACAGTGTTTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTG	3300
Qy	3301	GCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAG	3360

Db	3301		GCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAG	3360
Qy	3361		AAATCAGATGAAGGCCACCCATTAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAG	3420
Db	3361		AAATCAGATGAAGGCCACCCATTAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAG	3420
Qy	3421		GAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACATAAAAGAA	3480
Db	3421		GAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACATAAAAGAA	3480
Qy	3481		CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATG	3540
Db	3481		CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATG	3540
Qy	3541		TGGGTGTTTACTTATGTTGGTGCCTTGTTCATGGTCTGACACTACTGATTTTAGCTCTG	3600
Db	3541		TGGGTGTTTACTTATGTTGGTGCCTTGTTCATGGTCTGACACTACTGATTTTAGCTCTG	3600
Qy	3601		ATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTAT	3660
Db	3601		ATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTAT	3660
Qy	3661		CTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCT	3720
Db	3661		CTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCT	3720
Qy	3721		GGATTGAAGCGCAAAGCAGAT	3741
Db	3721		GGATTGAAGCGCAAAGCAGAT	3741

# RESULT 2

ABN86600

ID ABN86600 standard; DNA; 4684 BP.

XX

AC ABN86600;

XX

DT 05-NOV-2002 (first entry)

XX

DE Rat neurotransmitter receptor protein Nogo encoding DNA.

XX

KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;  
KW central nervous system; peripheral nervous system; tranquillizer; Nogo;  
KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;  
KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;  
KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;  
KW neurotransmitter receptor; rat; gene; ds.

XX

OS Rattus norvegicus.

XX

FH Key Location/Qualifiers

FT CDS 253. .3744

FT /\*tag= a

FT /product= "Nogo-A"

XX

PN US2002072493-A1.

XX  
 PD 13-JUN-2002.  
 XX  
 PF 28-JUN-2001; 2001US-00893348.  
 XX  
 PR 19-MAY-1998; 98IL-00124500.  
 PR 21-JUL-1998; 98WO-US014715.  
 PR 22-DEC-1998; 98US-00218277.  
 PR 19-MAY-1999; 99US-00314161.  
 XX  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 XX  
 PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;  
 PI Moalem G;  
 XX  
 DR WPI; 2002-607255/65.  
 DR P-PSDB; ABB81074, ABB81076, ABB81077.  
 XX  
 PT Promoting nerve regeneration and preventing neuronal degeneration in the  
 PT central/peripheral nervous system from injury/disease, comprises  
 PT administering nervous system-specific activated T cells/antigen, or  
 PT analogs/peptides.  
 XX  
 PS Disclosure; Page 40-44; 93pp; English.  
 XX  
 CC The invention relates to promoting nerve regeneration or conferring  
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the  
 CC central/peripheral nervous system (NS). The method involves administering  
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its  
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or  
 CC combinations. The method is useful for promoting nerve regeneration and  
 CC preventing neuronal degeneration in central/peripheral nervous system  
 CC from injury/disease, where the injury is spinal cord injury, blunt  
 CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or  
 CC damages caused by surgery such as tumour excision. The disease is not an  
 CC autoimmune disease or neoplasm. The disease results in a degenerative  
 CC process occurring in either gray or white matter or both. The disease is  
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's  
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,  
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and  
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such  
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral  
 CC neuropathies associated with various diseases, including but not limited  
 CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute  
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary  
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption  
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-  
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins  
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia  
 CC telangiectasia, Friedreich's ataxia, amyloid polyneuropathies,  
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's  
 CC disease, or lipoproteinemia. The present sequence represents a DNA  
 CC encoding the rat neurotransmitter receptor protein Nogo (Nogo-A, Nogo-B  
 CC and Nogo-C), an example of NS-specific antigen  
 XX  
 SQ Sequence 4684 BP; 1358 A; 1047 C; 1112 G; 1167 T; 0 U; 0 Other;

Query Match 100.0%; Score 3739.4; DB 6; Length 4684;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3740; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATTGCTCGTCTGGGCGGCGGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCG	60
Db	1	ATTGCTCGTCTGGGCGGCGGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCG	60
Qy	61	ATCGCGAAGGCAGCAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTT	120
Db	61	ATCGCGAAGGCAGGAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTT	120
Qy	121	CGGCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACA	180
Db	121	CGGCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACA	180
Qy	181	ACCGCCCGCGACTCTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGC	240
Db	181	ACCGCCCGCGACTCTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGC	240
Qy	241	GACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGC	300
Db	241	GACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGC	300
Qy	301	CCGCCCCGGCCTCCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAG	360
Db	301	CCGCCCCGGCCTCCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAG	360
Qy	361	GACGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTG	420
Db	361	GACGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTG	420
Qy	421	CTGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCCGCCGCCGCCGCG	480
Db	421	CTGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCCGCCGCCGCCGCG	480
Qy	481	CCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCCGGGCCGCTGCCGGCC	540
Db	481	CCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCCGGGCCGCTGCCGGCC	540
Qy	541	GCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCG	600
Db	541	GCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCG	600
Qy	601	CCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCT	660
Db	601	CCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCT	660
Qy	661	CCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCG	720
Db	661	CCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCG	720
Qy	721	CCCCCTTCCACGCCGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTT	780
Db	721	CCCCCTTCCACGCCGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTT	780
Qy	781	TTTGCTCTTCCTGCTGCATCTGAGCCTGTGATACCCTCCTCTGCAGAAAAAATTATGGAT	840

Db	781	 TTTGCTCTTCCTGCTGCATCTGAGCCTGTGATACCCTCCTCTGCAGAAAAATTATGGAT	840
Qy	841	TTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTG	900
Db	841	 TTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTG	900
Qy	901	CTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAA	960
Db	901	 CTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAA	960
Qy	961	CATGGATACCTTGGTAACTTATCAGCAGTGTCTCCTCAGAAGGAACAATTGAAGAACT	1020
Db	961	 CATGGATACCTTGGTAACTTATCAGCAGTGTCTCCTCAGAAGGAACAATTGAAGAACT	1020
Qy	1021	TTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGAT	1080
Db	1021	 TTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGAT	1080
Qy	1081	TTAGCAGAATTTTCAGAATTAGAATATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCA	1140
Db	1081	 TTAGCAGAATTTTCAGAATTAGAATATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCA	1140
Qy	1141	AAAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA	1200
Db	1141	 AAAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA	1200
Qy	1201	GACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCTGTGGGT	1260
Db	1201	 GACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCTGTGGGT	1260
Qy	1261	AAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATG	1320
Db	1261	 AAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATG	1320
Qy	1321	TCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGG	1380
Db	1321	 TCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGG	1380
Qy	1381	GAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTGGAA	1440
Db	1381	 GAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTGGAA	1440
Qy	1441	AGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAGTCTTGGGAAGGAT	1500
Db	1441	 AGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAGTCTTGGGAAGGAT	1500
Qy	1501	AGTGAAGGCAGAAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGACAGC	1560
Db	1501	 AGTGAAGGCAGAAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGACAGC	1560
Qy	1561	TCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACAGCAAAC	1620
Db	1561	 TCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACAGCAAAC	1620
Qy	1621	ACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAATAGAA	1680

Db	1621	ACTTTCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAAATAGAA	1680
Qy	1681	GAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTCCTT	1740
Db	1681	GAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTCCTT	1740
Qy	1741	GTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACT	1800
Db	1741	GTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACT	1800
Qy	1801	GAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGCATGT	1860
Db	1801	GAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGCATGT	1860
Qy	1861	GAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTG	1920
Db	1861	GAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTG	1920
Qy	1921	GTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTGCCCATCA	1980
Db	1921	GTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTGCCCATCA	1980
Qy	1981	TTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTGCCTGATATTGTTATGGAAGCACCA	2040
Db	1981	TTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTGCCTGATATTGTTATGGAAGCACCA	2040
Qy	2041	TTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCACTG	2100
Db	2041	TTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCACTG	2100
Qy	2101	GAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCACCA	2160
Db	2101	GAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCACCA	2160
Qy	2161	TATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAG	2220
Db	2161	TATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAG	2220
Qy	2221	CCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGT	2280
Db	2221	CCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGT	2280
Qy	2281	GATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTCA	2340
Db	2281	GATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTCA	2340
Qy	2341	GAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCCCTCA	2400
Db	2341	GAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCCCTCA	2400
Qy	2401	CCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCCTGAAGTCCCACAAACA	2460
Db	2401	CCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCCTGAAGTCCCACAAACA	2460
Qy	2461	CAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCC	2520
Db	2461	CAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCC	2520

Qy	2521	CAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAGCCATATTTAGAG	2580
Db	2521	CAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAGCCATATTTAGAG	2580
Qy	2581	TCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTG	2640
Db	2581	TCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTG	2640
Qy	2641	ACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTAATACTGCAATTTATTCAAAT	2700
Db	2641	ACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTAATACTGCAATTTATTCAAAT	2700
Qy	2701	GATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCA	2760
Db	2701	GATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCA	2760
Qy	2761	TCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTGAGTGCTAAAGATGATTCTCCT	2820
Db	2761	TCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTGAGTGCTAAAGATGATTCTCCT	2820
Qy	2821	AAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATC	2880
Db	2821	AAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATC	2880
Qy	2881	CAAAGCGGGCAGATTTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAAAT	2940
Db	2881	CAAAGCGGGCAGATTTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAAAT	2940
Qy	2941	ATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTA	3000
Db	2941	ATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTA	3000
Qy	3001	TCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGC	3060
Db	3001	TCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGC	3060
Qy	3061	AGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACA	3120
Db	3061	AGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACA	3120
Qy	3121	GAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACCTTCAGTT	3180
Db	3121	GAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACCTTCAGTT	3180
Qy	3181	GTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTA	3240
Db	3181	GTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTA	3240
Qy	3241	TTCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTG	3300
Db	3241	TTCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTG	3300
Qy	3301	GCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAG	3360
Db	3301	GCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAG	3360

Qy	3361	AAATCAGATGAAGGCCACCCATT	CAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAG	3420
Db	3361	AAATCAGATGAAGGCCACCCATT	CAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAG	3420
Qy	3421	GAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAGAA		3480
Db	3421	GAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAGAA		3480
Qy	3481	CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATG		3540
Db	3481	CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATG		3540
Qy	3541	TGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTG		3600
Db	3541	TGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTG		3600
Qy	3601	ATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTAT		3660
Db	3601	ATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTAT		3660
Qy	3661	CTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCT		3720
Db	3661	CTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCT		3720
Qy	3721	GGATTGAAGCGCAAAGCAGAT		3741
Db	3721	GGATTGAAGCGCAAAGCAGAT		3741

RESULT 3

AAS09453

ID AAS09453 standard; cDNA; 4053 BP.

XX

AC AAS09453;

XX

DT 26-SEP-2001 (first entry)

XX

DE Human cDNA encoding the Nogo protein.

XX

KW Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein;

KW cranial trauma; cerebral trauma; spinal cord injury; stroke;

KW demyelinating disease; multiple sclerosis; monophasis demyelination;

KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis;

KW Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy;

KW Pelizaeus-Merzbacher disease; Spongy degeneration; Alexander's disease;

KW Canavan's disease; metachromatic leukodystrophy; viral infection;

KW Krabbe's disease; AB020693; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 135..3713

FT /\*tag= a

FT /product= "Nogo protein"

XX

PN WO200151520-A2.

XX



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PD      19-JUL-2001.
XX
XX
PF      12-JAN-2001; 2001WO-US001041.
XX
PR      12-JAN-2000; 2000US-0175707P.
PR      26-MAY-2000; 2000US-0207366P.
PR      29-SEP-2000; 2000US-0236378P.
XX
PA      (UYYA ) UNIV YALE.
XX
PI      Strittmatter SM;
XX
DR      WPI; 2001-442138/47.
DR      P-PSDB; AAU09453.
XX
PT      Novel Nogo receptor protein useful for identifying modulator of Nogo
PT      protein or Nogo receptor protein, which is useful for treating central
PT      nervous system disorders.
XX
PS      Example 1; Page 95-100; 109pp; English.
XX
CC      The sequence (Genbank accession number AB0202693) encodes the human Nogo
CC      protein, a 250kDa myelin-associated axon growth inhibitor. The invention
CC      relates to the use of the nogo receptor, nogo protein, their nucleic
CC      acids, vectors expressing them and antibodies against them, to isolate
CC      agents which block nogo receptor mediated axonal growth. The agent is
CC      useful for treating a central nervous system disorder which is a result
CC      of cranial or cerebral trauma, spinal cord injury, stroke or a
CC      demyelinating disease selected from multiple sclerosis, monophasis
CC      demyelination, encephalomyelitis, multifocal leukoencephalopathy,
CC      panencephalitis, Marchiafava-Bignami disease, pontine myelinolysis,
CC      adrenoleukodystrophy, Pelizaeus-Merzbacher disease, Spongy degeneration,
CC      Alexander's disease, Canavan's disease, metachromatic leukodystrophy,
CC      viral infection and Krabbe's disease
XX
SQ      Sequence 4053 BP; 1189 A; 922 C; 922 G; 1020 T; 0 U; 0 Other;

Query Match          62.6%; Score 2343.6; DB 4; Length 4053;
Best Local Similarity 81.3%; Pred. No. 0;
Matches 3017; Conservative 0; Mismatches 574; Indels 119; Gaps 21;

Qy      134 CACGACTCGGCCTGCCTGGCCCCTGCCAGTCTTGCCCCAACCCCCACAACCGCCCGCGACT 193
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      16 CTCGGCTCAGTCGGCCAGCCCTCTCAGTCCTCCCCAACCCCCACAACCGCCCGCGGCT 75

Qy      194 CTGAGGAGAAGCGGC-CCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCC 252
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      76 CTGAGACGCGGCCCCGGCGGCGGCGGCAGCAGCTGCAGCATCATC-TCCACCCTCCAGCC 134

Qy      253 ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCCT 312
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      135 ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCTCTGGACAGCCACCCCGGCCG 191

Qy      313 CCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG 372
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      192 CAGCCCGCGTTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 248

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Qy	373	GAGGAGGACGAGGAGGAGGAGGACGAGGACCTAGAGGAACCTGGAGGTGCTGGAGAGGAAG	432
Db	249	GAGGAGGAAGAGGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG	308
Qy	433	CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCCGCCGCCGCCGCCGCTG	486
Db	309	CCCGCCGCCGGGCTGTCCGCGGCCCCAGTGCCACCGCCCCCTGCCGCCGGCGGCCCCCTG	368
Qy	487	CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCC	546
Db	369	ATGGACTTCGGAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC	428
Qy	547	CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC	597
Db	429	CCCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCTGTCGACCGTGCCC	488
Qy	598	GCGCCATCCCTGCCGCCCGCTGCCGCGAGTCTGCCCTCCAAGCTCCCAGAGGACGACGAG	657
Db	489	GCGCCATCCCCGCTGTCTGCTGCCGCGAGTCTGCCCTCCAAGCTCCCTGAGGACGACGAG	548
Qy	658	CCTCCGGCGAGGCCCCCGCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG-----	711
Db	549	CCTCCGGCCCCGGCCTCCCCCTCCTCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG	608
Qy	712	-----CCCCGCCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC	750
Db	609	TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCCGCCGCGCCCAAGCGC	668
Qy	751	AGGGGCTCC---GGCTCAGTGGATGAGACCCCTTTTGTCTCTTCCTGCTGCATCTGAGCCT	807
Db	669	AGGGGCTCCTCGGGCTCAGTGGATGAGACCCCTTTTGTCTCTTCCTGCTGCATCTGAGCCT	728
Qy	808	GTGATACCCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT	867
Db	729	GTGATACGCTCCTCTGCAGAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT	785
Qy	868	TCGTCTGGTCAAGAGGATTTCCCATCTGTCTTGAACTGCTGCCTCTCTTCCTTCT	927
Db	786	TCGGCTGGTCAAGAGGATTTCCCATCTGTCTTGAACTGCTGCTTCTCTTCCTTCT	845
Qy	928	CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACCTTATCAGCA	987
Db	846	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	905
Qy	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Db	906	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	965
Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Db	966	GAGAAGGCAAAAACCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC	1025
Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Db	1026	TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	1085
Qy	1168	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT	1224

Db 1086 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1145  
 Qy 1225 GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC 1269  
 Db 1146 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1205  
 Qy 1270 AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA 1329  
 Db 1206 GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGAA 1265  
 Qy 1330 GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA 1389  
 Db 1266 GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA 1325  
 Qy 1390 GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG 1437  
 Db 1326 GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG 1382  
 Qy 1438 GAAAGTAAAGTGGACAGAAAATGCTTGGAAAGATAGCCTGGAGCAAAAAGTCTTGGGAAG 1497  
 Db 1383 GAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACCTAATCACGAAAA 1442  
 Qy 1498 GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC 1557  
 Db 1443 GATAGTGAAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT 1502  
 Qy 1558 AGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACCACA 1614  
 Db 1503 CGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA 1562  
 Qy 1615 GCAAACACTTTCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAA 1674  
 Db 1563 ACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAAA 1622  
 Qy 1675 ATAGAAGAAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT 1731  
 Db 1623 ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAAC 1682  
 Qy 1732 CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA 1791  
 Db 1683 CCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA 1742  
 Qy 1792 AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG 1851  
 Db 1743 AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG 1802  
 Qy 1852 GAAGCATGTGAAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA 1911  
 Db 1803 GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA 1862  
 Qy 1912 GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT 1971  
 Db 1863 ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT 1922  
 Qy 1972 TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCAACAGTTTTGCCTGATATTGTTATG 2031

Db	1923	TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG	1982
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA	2091
Db	1983	GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA	2042
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Db	2043	TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	2099
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	2100	CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA	2159
Qy	2209	GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTCAAGGAAACAGAAGCTCCTTATATA	2268
Db	2160	GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA	2219
Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTC	2328
Db	2220	TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTCTGCTGAACCAGCTCCGGATTTC	2279
Qy	2329	TCTAATTATTTCAGAAATAGCAAAATTCGAGAAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Db	2280	TCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2339
Qy	2389	GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTGAA	2448
Db	2340	GAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2399
Qy	2449	GTCCCACAAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2400	GTTCCACAAAACACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2459
Qy	2503	GTGTCTGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
Db	2460	TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA	2519
Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
Db	2520	GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA	2579
Qy	2620	TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTT	2679
Db	2580	CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTC	2639
Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA	2739
Db	2640	AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2699
Qy	2740	AGTGAAACATTTTCAGATTCTCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC	2799
Db	2700	ACTGAAACGTTTTTCAGATTCTCTCAATTGAAATTATAGATGAGTTCCTACATTGATC	2759
Qy	2800	AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC	2856
Db	2760	AGTTCTAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC	2819

Qy	2857	GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCAATTGCCTTGCTTAGAATTG	2916
Db	2820	CACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCAATTGCCTTGCACAGAATTG	2879
Qy	2917	CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA	2970
Db	2880	CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA	2939
Qy	2971	GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC	3030
Db	2940	GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT	2999
Qy	3031	TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA	3090
Db	3000	TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA	3059
Qy	3091	GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA	3150
Db	3060	GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	3119
Qy	3151	TTGTCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG	3210
Db	3120	TTTTCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG	3179
Qy	3211	AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTACGC	3270
Db	3180	AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGC	3239
Qy	3271	ATTGTGAGCGTAAACAGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG	3330
Db	3240	ATTGTGAGCGTAAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG	3299
Qy	3331	ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTACAGGGCA	3390
Db	3300	ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTACAGGGCA	3359
Qy	3391	TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTTCAGAAATACAGTAATTCTGCT	3450
Db	3360	TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGTAATTCTGCT	3419
Qy	3451	CTTGGTCATGTGAACAGCACAAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA	3510
Db	3420	CTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA	3479
Qy	3511	GTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT	3570
Db	3480	GTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT	3539
Qy	3571	AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT	3630
Db	3540	AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT	3599
Qy	3631	GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT	3690
Db	3600	GAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAGAT	3659

Qy 3691 GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740  
 || ||||| |||||||||||||||||||||||||||||||||||| ||  
 Db 3660 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3709

RESULT 4

ACC81048

ID ACC81048 standard; cDNA; 4053 BP.

XX

AC ACC81048;

XX

DT 22-JUL-2003 (first entry)

XX

DE Human NogoA gene.

XX

KW Human; Nogo receptor; NgR; CTS domain; neuroprotective; gene therapy;  
 KW axonal growth; central nervous system; CNS; Nogo; spinal cord injury;  
 KW cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;  
 KW demyelinating disease; multiple sclerosis; monophasic demyelination;  
 KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; gene;  
 KW ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 135..3713

FT /\*tag= a

FT /product= "Human NogoA"

XX

PN WO2003031462-A2.

XX

PD 17-APR-2003.

XX

PF 04-OCT-2002; 2002WO-US032007.

XX

PR 06-OCT-2001; 2001US-00972599.

XX

PA (UYYA ) UNIV YALE.

XX

PI Strittmatter SM;

XX

DR WPI; 2003-393433/37.

DR P-PSDB; ABR59667.

XX

PT New human Nogo receptor polypeptides and nucleic acids, useful for  
 PT decreasing inhibition of axonal growth by a central nervous system  
 PT neuron, or in treating central nervous system disease, disorder or  
 PT injury, e.g. spinal cord injury.

XX

PS Disclosure; Page 126-131; 148pp; English.

XX

CC The invention relates to a novel nucleic acid encoding a polypeptide  
 CC comprising amino acid residues 27-309 of a 473 amino acid sequence (P1,  
 CC human Nogo receptor (NgR) NTLRRCT domain), or residues 27-309 of P1 with  
 CC 1-20 conservative amino acid substitutions, and less than a complete CTS  
 CC domain, provided that a partial CTS domain, if present, consists of no  
 CC more than the first 39 consecutive residues. The nucleic acid of the



Db 549 CCTCCGGCCCCGGCCTCCCCCTCCTCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG 608  
 Qy 712 -----CCCCGCCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC 750  
 Db 609 TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCGGCCGCGCCCAAGCGC 668  
 Qy 751 AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 807  
 Db 669 AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 728  
 Qy 808 GTGATACCCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT 867  
 Db 729 GTGATACGCTCCTCTGCAGAAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT 785  
 Qy 868 TCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCCTTCT 927  
 Db 786 TCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCTTCTCTTCCTTCT 845  
 Qy 928 CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACCTATCAGCA 987  
 Db 846 CTGTCTCCTCTCTCAGCCGCTTCTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 905  
 Qy 988 GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA 1047  
 Db 906 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 965  
 Qy 1048 GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT 1107  
 Db 966 GAGAAGGCAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC 1025  
 Qy 1108 TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA 1167  
 Db 1026 TCAGAAATGGGATCATCGTTTCAAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 1085  
 Qy 1168 AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT 1224  
 Db 1086 AATCCTAGGGAAGAAATAATCGTGAAAAATAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1145  
 Qy 1225 GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC 1269  
 Db 1146 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1205  
 Qy 1270 AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTAATGAAATGCAGATGTCAGTAGTA 1329  
 Db 1206 GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTGGAA 1265  
 Qy 1330 GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA 1389  
 Db 1266 GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA 1325  
 Qy 1390 GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG 1437  
 Db 1326 GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG 1382  
 Qy 1438 GAAAGTAAAGTGGACAGAAAATGCTTGGGAAGATAGCCTGGAGCAAAAAGTCTTGGGAAG 1497  
 Db 1383 GAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACTAATCACGAAAAA 1442



Qy 1498 GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGAC 1557  
 ||||| | || |||| | || ||||| ||||| ||||| | |||||  
 Db 1443 GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT 1502

Qy 1558 AGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACCACA 1614  
 | || ||||| || ||||| ||||| | ||||| || ||||| ||  
 Db 1503 CGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA 1562

Qy 1615 GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAA 1674  
 ||||| || ||||| ||||| ||||| ||||| || ||||| |||||  
 Db 1563 ACAAACATTTTCCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAAA 1622

Qy 1675 ATAGAAGAAAGGAAGGCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT 1731  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1623 ATAGAAGAAAAGAAGGCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAAC 1682

Qy 1732 CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA 1791  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1683 CCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA 1742

Qy 1792 AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG 1851  
 ||||| ||||| || || ||||| ||||| ||||| ||||| |||||  
 Db 1743 AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG 1802

Qy 1852 GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA 1911  
 ||||| ||||| ||||| ||||| || ||||| ||||| ||||| |||||  
 Db 1803 GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA 1862

Qy 1912 GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT 1971  
 ||||| ||||| ||||| ||||| || ||||| ||||| || || |||||  
 Db 1863 ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT 1922

Qy 1972 TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG 2031  
 ||||| ||||| || || ||||| ||||| ||||| ||||| |||||  
 Db 1923 TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG 1982

Qy 2032 GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCAGTGTA 2091  
 ||||| ||||| ||||| || ||||| ||||| || || ||||| ||  
 Db 1983 GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCAGCTCA 2042

Qy 2092 TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC 2151  
 || ||| | |||| || || ||||| ||||| || ||||| | |||||  
 Db 2043 TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC 2099

Qy 2152 CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA 2208  
 ||||| ||||| ||||| ||||| ||||| | ||| |||||  
 Db 2100 CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA 2159

Qy 2209 GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA 2268  
 | ||| ||||| ||||| | ||||| ||||| ||||| ||||| |||||  
 Db 2160 GAAATTAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA 2219

Qy 2269 TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC 2328  
 || ||||| ||||| ||||| ||||| || ||||| || |||||  
 Db 2220 TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTTC 2279

[illegible]

Db	3120	TTTTTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG	3179
Qy	3211	AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGC	3270
Db	3180	AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTTCATTGACAGTATTCAGC	3239
Qy	3271	ATTGTCAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG	3330
Db	3240	ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG	3299
Qy	3331	ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA	3390
Db	3300	ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA	3359
Qy	3391	TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT	3450
Db	3360	TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAAGTACAGTAATTCTGCT	3419
Qy	3451	CTTGATCATGTGAACAGCACATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA	3510
Db	3420	CTTGATCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA	3479
Qy	3511	GTTGATTCCCTGAAGTTTGCACTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT	3570
Db	3480	GTTGATTCTCTGAAGTTTGCACTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT	3539
Qy	3571	AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT	3630
Db	3540	AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT	3599
Qy	3631	GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT	3690
Db	3600	GAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT	3659
Qy	3691	GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA	3740
Db	3660	GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA	3709

RESULT 5

ABV94680

ID ABV94680 standard; cDNA; 4632 BP.

XX

AC ABV94680;

XX

DT 14-JAN-2003 (first entry)

XX

DE Human pancreatic cancer expressed cDNA SEQ ID NO 53.

XX

KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;  
KW cytostatic; tumour; gene; ss.

XX

OS Homo sapiens.

XX

PN WO200260317-A2.

XX



Db 83 CTGAGACGCGGCCCCGGCGGGCGGCAGCAGCTGCAGCATCATC-TCCACCCTCCAGCC 141  
 Qy 253 ATGGAAGACATAGACCAGTCGTGCTGGTCTCCTCGTCCACGGACAGCCCCGCCCCGGCCT 312  
 ||||| | ||||| | |||| | ||||| ||||| ||||| |||||  
 Db 142 ATGGAAGACCTGGACCAGTCCTCTGGT---CTCGTCTCGGACAGCCCACCCCGGCCG 198  
 Qy 313 CCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCCGAGGACGAGGAGGACGAGGAGGAG 372  
 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 199 CAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCCGAGGACGAGGAG---GAAGAAGAG 255  
 Qy 373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG 432  
 ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||  
 Db 256 GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG 315  
 Qy 433 CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCGCCGCCGCCGCGCCGCTG 486  
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 Db 316 CCCGCCGCGGGCTGTCCGCGGCCCACTGCCACCGCCCTGCCGCCGGCGCGCCCTG 375  
 Qy 487 CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCC 546  
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 Db 376 ATGGACTTCGGAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC 435  
 Qy 547 CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC 597  
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 Db 436 CCCGTCGCCCCGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCTGTCGACCGTGCCC 495  
 Qy 598 GCGCCATCCCTGCCGCCCGCTGCCGCAGTCTTGCCTCCAAGCTCCCAGAGGACGACGAG 657  
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 Db 496 GCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG 555  
 Qy 658 CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG----- 711  
 ||||| |||| || ||||| || || || ||||| ||||| ||||| |||||  
 Db 556 CCTCCGGCCCCGCCTCCCCCTCCTCCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG 615  
 Qy 712 -----CCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC 750  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 616 TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCGCGCCGCGCCCAAGCGC 675  
 Qy 751 AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 807  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 676 AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 735  
 Qy 808 GTGATACCCTCCTCTGCAGAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT 867  
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 Db 736 GTGATACGCTCCTCTGCAGAAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT 792  
 Qy 868 TCGTCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAACTGCTGCCTCTCTTCCTTCT 927  
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 Db 793 TCGGCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAACTGCTGCTTCTCTTCCTTCT 852  
 Qy 928 CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACCTTATCAGCA 987  
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 Db 853 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 912  
 Qy 988 GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA 1047  
 || | || | ||||| || ||||| | | ||||| ||||| ||||| ||||| |||||  
 Db 913 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 972

Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Db	973	GAGAAGGCAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC	1032
Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Db	1033	TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	1092
Qy	1168	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT	1224
Db	1093	AATCCTAGGGAAGAAATAATCGTGAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1152
Qy	1225	GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC	1269
Db	1153	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1212
Qy	1270	AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA	1329
Db	1213	GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGAA	1272
Qy	1330	GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA	1389
Db	1273	GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA	1332
Qy	1390	GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG	1437
Db	1333	GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG	1389
Qy	1438	GAAAGTAAAGTGGACAGAAAATGCTTGGGAAGATAGCCTGGAGCAAAAAAGTCTTGGAAG	1497
Db	1390	GAAAGTAAAGTGGATAAAAAATGTTTGCAGATAGCCTTGAGCAAACTAATCACGAAAAA	1449
Qy	1498	GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCGAGTACCCAGAACCTGTGAAGGAC	1557
Db	1450	GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCGAGTACGCCAGAAGGTATAAAGGAT	1509
Qy	1558	AGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACCACA	1614
Db	1510	CGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA	1569
Qy	1615	GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA	1674
Db	1570	ACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAA	1629
Qy	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT	1731
Db	1630	ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAAC	1689
Qy	1732	CCTTTCCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Db	1690	CCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA	1749
Qy	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG	1851
Db	1750	AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG	1809

Qy	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Db	1810	GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA	1869
Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Db	1870	ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT	1929
Qy	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	2031
Db	1930	TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG	1989
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA	2091
Db	1990	GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA	2049
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Db	2050	TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	2106
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	2107	CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA	2166
Qy	2209	GGAATAAAAGAGCCTGAAAGTTTAAATGCAGCTGTTCAAGAAACAGAAGCTCCTTATATA	2268
Db	2167	GAAATTAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA	2226
Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTT	2328
Db	2227	TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTT	2286
Qy	2329	TCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Db	2287	TCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2346
Qy	2389	GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTGATTCTCCTGAA	2448
Db	2347	GAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2406
Qy	2449	GTCCACACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2407	GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2466
Qy	2503	GTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
Db	2467	TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA	2526
Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
Db	2527	GGAAAGCCATATTTGGAATCTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA	2586
Qy	2620	TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTT	2679
Db	2587	CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTC	2646
Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAGAA	2739

Db	2647	AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2706
Qy	2740	AGTGAAACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTG	2799
Db	2707	ACTGAAACGTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTTCCTTACATTGATC	2766
Qy	2800	AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC	2856
Db	2767	AGTTCTAAAACGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC	2826
Qy	2857	GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTG	2916
Db	2827	CACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCATTGCCTTGACACAGAATTG	2886
Qy	2917	CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA	2970
Db	2887	CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA	2946
Qy	2971	GATGAATTCTCCGAAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC	3030
Db	2947	GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT	3006
Qy	3031	TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA	3090
Db	3007	TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA	3066
Qy	3091	GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA	3150
Db	3067	GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	3126
Qy	3151	TTGTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG	3210
Db	3127	TTTTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG	3186
Qy	3211	AAGACTGGAGTGGTGTGTTGGTGCCAGCCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGC	3270
Db	3187	AAGACTGGAGTGGTGTGTTGGTGCCAGCCTTATTCCTGCTGCTTTTATTGACAGTATTGAGC	3246
Qy	3271	ATTGTGAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG	3330
Db	3247	ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG	3306
Qy	3331	ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCA	3390
Db	3307	ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCA	3366
Qy	3391	TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT	3450
Db	3367	TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT	3426
Qy	3451	CTTGGTCATGTGAACAGCACATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA	3510
Db	3427	CTTGGTCATGTGAAGTGCACGATAAAGGAACTGAGGCGCCTCTTCTTAGTTGATGATTTA	3486
Qy	3511	GTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT	3570



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Db      3487 GTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT 3546
Qy      3571 AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT 3630
        ||||||||||||||||||||| |||| | | ||||||||||| |||||||||||||
Db      3547 AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACCTCTTCAGTGTTCCTGTTATTTAT 3606
Qy      3631 GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTAAAGGAT 3690
        ||||||||||| ||||||||||||||||||||||||| ||| ||||| |||
Db      3607 GAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT 3666
Qy      3691 GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
        || ||||| ||||||||||||||||||||||||||||| |||
Db      3667 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3716

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RESULT 6

AAA23454

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ID  AAA23454 standard; cDNA; 4093 BP.
XX
AC  AAA23454;
XX
DT  19-JUN-2000 (first entry)
XX
DE  cDNA encoding human secreted protein vb22_1, SEQ ID NO:63.
XX
KW  Human; secreted protein; cancer; tumour; cardiovascular disorder;
KW  blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;
KW  infection; fungal; bacterial; viral; HIV; allergy; arthritis;
KW  neurodegenerative disease; asthma; contraceptive; ss.
XX
OS  Homo sapiens.
XX
FH  Key          Location/Qualifiers
FT  CDS          152..1006
FT              /*tag= b
FT              /product= "Clone vb22_1 ORF2"
FT  CDS          1048..3729
FT              /*tag= a
FT              /product= "Human secreted protein vb22_1"
XX
PN  WO200011015-A1.
XX
PD  02-MAR-2000.
XX
PF  24-AUG-1999; 99WO-US019351.
XX
PR  24-AUG-1998; 98US-0097638P.
PR  24-AUG-1998; 98US-0097659P.
PR  09-SEP-1998; 98US-0099618P.
PR  28-SEP-1998; 98US-0102092P.
PR  25-NOV-1998; 98US-0109978P.
PR  23-DEC-1998; 98US-0113645P.
PR  23-DEC-1998; 98US-0113646P.
PR  23-AUG-1999; 99US-00379246.
XX
PA  (ALPH-) ALPHAGENE INC.
XX

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PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;

XX

DR WPI; 2000-224657/19.

DR P-PSDB; AAY95012, AAY95030.

XX

PT New secreted or transmembrane proteins and polynucleotides encoding them,  
PT useful for treating neurodegenerative disorders, autoimmune diseases and  
PT cancer.

XX

PS Claim 72; Page 321-322; 357pp; English.

XX

CC The invention relates to 40 human secreted proteins (AAY94981-Y95020),  
CC and cDNA sequences encoding them (AAA23423-A23462). The secreted proteins  
CC of the invention include those that are thought to be only partially  
CC secreted, i.e., transmembrane proteins. The proteins of the invention may  
CC exhibit one or more activities selected from the following: cytokine  
CC activity; cell proliferation; differentiation; immune modulation;  
CC haematopoiesis regulation; tissue growth activity; activin/inhibin  
CC activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic  
CC activity; anti-inflammatory activity; and tumour inhibition activity. The  
CC proteins may be administered to patients as vaccines, and the nucleotides  
CC may be used as part of a gene therapy regime. Diseases or conditions that  
CC may be treated using the proteins or nucleotides of the invention include  
CC autoimmune diseases; genetic disorders; haemophilia; cardiovascular  
CC diseases; cancer; bacterial, fungal and viral infections, especially HIV;  
CC multiple sclerosis; rheumatoid arthritis; pulmonary inflammation;  
CC Guillain-Barre syndrome; insulin dependent diabetes mellitus; and  
CC allergic reactions such as asthma and anaemia. They may also be used for  
CC treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal  
CC diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease  
CC and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin  
CC activity may additionally be useful as contraceptives. Nucleic acid  
CC sequences of the invention may be used in chromosome mapping, and as a  
CC source of diagnostic primers and probes. The present sequence represents  
CC cDNA encoding one of the 40 proteins of the invention

XX

SQ Sequence 4093 BP; 1213 A; 926 C; 928 G; 1026 T; 0 U; 0 Other;

Query Match 62.4%; Score 2333.2; DB 3; Length 4093;

Best Local Similarity 81.3%; Pred. No. 0;

Matches 3017; Conservative 0; Mismatches 573; Indels 120; Gaps 22;

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QY      134 CACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACAACCGCCCGCGACT 193
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Db      33 CTCGGCTCAGTCGGCCCAGCCCCTCTCAGTCCTCCCAACCCCCACAACCGCCCGCGGGCT 92

QY      194 CTGAGGAGAAGCGGC-CCTGCGGCGGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCC 252
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      93 CTGAGACGCGGCCCCGGCGGGCGGGCAGCAGCTGCAGCATCATC-TCCACCCCTCCAGCC 151

QY      253 ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCT 312
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      152 ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCCTCGGACAGCCACCCCGGCCG 208

QY      313 CCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCAGGACGAGGAGGACGAGGAGGAG 372
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Db      209 CAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCAGGACGAGGAG---GAAGAAGAG 265
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Qy	373	GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG	432
Db	266	GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG	325
Qy	433	CCCGCAGCCGGGCTGTCCGAGCTGCGGTGC-----CGCCCCGCCGCCGCCGCCGCTG	486
Db	326	CCCGCCGCCGGGCTGTCCGCGGCCCCAGTGCCACCGCCCCCTGCCGCCGGCGCGCCCTG	385
Qy	487	CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCC	546
Db	386	ATGGACTTCGAAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC	445
Qy	547	CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC	597
Db	446	CCCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTCGACCGTGCCC	505
Qy	598	GCGCCATCCCTGCCGCCCGCTGCCGCAGTCTGCCCTCCAAGCTCCAGAGGACGACGAG	657
Db	506	GCGCCATCCCGCTGTCTGCTGCCGCAGTCTGCCCTCCAAGCTCCCTGAGGACGACGAG	565
Qy	658	CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG-----	711
Db	566	CCTCCGGCCCGCCTCCCCCTCCTCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG	625
Qy	712	-----CCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC	750
Db	626	TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCGGCCGCGCCCAAGCGC	685
Qy	751	AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTTGCTCTTCTGCTGCATCTGAGCCT	807
Db	686	AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTTCTGCTGCATCTGAGCCT	745
Qy	808	GTGATACCCTCCTCTGCAGAAAAATTATGGATTGATGGAGCAGCCAGGTAACACTGTT	867
Db	746	GTGATACGCTCCTCTGCAGAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT	802
Qy	868	TCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAACTGCTGCCTCTCTCCTTCT	927
Db	803	TCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAACTGCTGCTTCTCTCCTTCT	862
Qy	928	CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGAACCTATCAGCA	987
Db	863	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGAATTTGTCAACA	922
Qy	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Db	923	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	982
Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Db	983	GAGAAGGCAA--AACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC	1041
Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Db	1042	TCAGAAATGGGATCATCGTTTCAAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	1101

Qy 1168 AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT 1224  
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 Db 1102 AATCCTAGGGAAGAAATAATCGTGAAAAATAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1161

Qy 1225 GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC 1269  
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 Db 1162 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1221

Qy 1270 AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTTAATGAAATGCAGATGTCAGTAGTA 1329  
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 Db 1222 GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTGGAA 1281

Qy 1330 GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA 1389  
 || ||| ||||| || ||||| ||||| || ||||| || || ||||| |||||  
 Db 1282 GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA 1341

Qy 1390 GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG 1437  
 |||| | ||| | ||| ||| || ||||| ||| | || ||  
 Db 1342 GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG 1398

Qy 1438 GAAAGTAAAGTGGACAGAAAATGCTTGAAGATAGCCTGGAGCAAAAAAGTCTTGGGAAG 1497  
 ||||| ||||| | ||||| || | ||||| ||||| | || | ||  
 Db 1399 GAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAAAAA 1458

Qy 1498 GATAGTGAAGGCAGAAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC 1557  
 ||||| | || ||||| || ||||| ||||| ||||| | | |||||  
 Db 1459 GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT 1518

Qy 1558 AGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACCACA 1614  
 | || ||||| || ||||| |||| | ||||| || |||| ||  
 Db 1519 CGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA 1578

Qy 1615 GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA 1674  
 ||||| || ||||| |||| ||||| ||||| || ||||| |||||  
 Db 1579 ACAAACATTTTCCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAA 1638

Qy 1675 ATAGAAGAAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT 1731  
 ||||| || ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1639 ATAGAAGAAAAGGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAAC 1698

Qy 1732 CCTTTCCTTGTCAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA 1791  
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 Db 1699 CCTTTCCTTGTCAGCAGCAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA 1758

Qy 1792 AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG 1851  
 ||||| || || ||||| ||||| ||||| ||||| |||||  
 Db 1759 AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG 1818

Qy 1852 GAAGCATGTGAAAGTGAATGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA 1911  
 ||||| ||||| ||||| || ||||| ||||| ||||| |||||  
 Db 1819 GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA 1878

Qy 1912 GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT 1971  
 ||||| ||||| ||||| || ||||| ||||| || || ||||| |||||  
 Db 1879 ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT 1938

Qy 1972 TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG 2031

Db	1939		TGCCCATCATTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG	1998
Qy	2032		GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCAGTGTA	2091
Db	1999		GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCAGCTCA	2058
Qy	2092		TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Db	2059		TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	2115
Qy	2152		CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	2116		CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA	2175
Qy	2209		GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268
Db	2176		GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA	2235
Qy	2269		TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC	2328
Db	2236		TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTTC	2295
Qy	2329		TCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Db	2296		TCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2355
Qy	2389		GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCTGAA	2448
Db	2356		GAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCGAATACCTGAC	2415
Qy	2449		GTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2416		GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2475
Qy	2503		GTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCCTCACCTCAGGAGCTA	2562
Db	2476		TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAAAGTCACTGCTTTGCCACCTGAGGGA	2535
Qy	2563		GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
Db	2536		GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA	2595
Qy	2620		TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTT	2679
Db	2596		CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAGCTC	2655
Qy	2680		AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA	2739
Db	2656		AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2715
Qy	2740		AGTGAAACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC	2799
Db	2716		ACTGAAACGTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATC	2775
Qy	2800		AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC	2856

Db 2776 AGTTCTAAAAC TGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC 2835  
 Qy 2857 GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTG 2916  
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 Db 2836 CACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTTCATTGCCTTGACACAGAATTG 2895  
 Qy 2917 CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA 2970  
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 Db 2896 CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA 2955  
 Qy 2971 GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC 3030  
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 Db 2956 GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT 3015  
 Qy 3031 TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA 3090  
 |||||  
 Db 3016 TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA 3075  
 Qy 3091 GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA 3150  
 |||||  
 Db 3076 GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA 3135  
 Qy 3151 TTGTCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG 3210  
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 Db 3136 TTTTCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG 3195  
 Qy 3211 AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTCA 3270  
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 Db 3196 AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTTCATTGACAGTATTCAGC 3255  
 Qy 3271 ATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG 3330  
 |||||  
 Db 3256 ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG 3315  
 Qy 3331 ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA 3390  
 |||||  
 Db 3316 ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA 3375  
 Qy 3391 TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT 3450  
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 Db 3376 TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT 3435  
 Qy 3451 CTTGGTCATGTGAACAGCACAAATAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA 3510  
 |||||  
 Db 3436 CTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA 3495  
 Qy 3511 GTTGATTCCCTGAAGTTTGCACTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT 3570  
 |||||  
 Db 3496 GTTGATTCTCTGAAGTTTGCACTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT 3555  
 Qy 3571 AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT 3630  
 |||||  
 Db 3556 AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT 3615  
 Qy 3631 GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT 3690  
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 Db 3616 GAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT 3675

Qy 3691 GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740  
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 Db 3676 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3725

RESULT 7

ABS70449

ID ABS70449 standard; cDNA; 4822 BP.

XX

AC ABS70449;

XX

DT 27-NOV-2002 (first entry)

XX

DE Human bone remodelling gene #106.

XX

KW Bone remodelling; osteoporosis; human; gene; ss.

XX

OS Homo sapiens.

XX

PN US6426186-B1.

XX

PD 30-JUL-2002.

XX

PF 18-JAN-2000; 2000US-00484970.

XX

PR 18-JAN-2000; 2000US-00484970.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Jones KA, Volkmuth W, Walker MG;

XX

DR WPI; 2002-673014/72.

XX

PT A combination of polynucleotides which are co-expressed with genes known  
 PT to be involved in bone remodeling and osteoporosis are useful in an array  
 PT for the diagnosis of bone remodeling and osteoporosis associated  
 PT disorders.

XX

PS Claim 1; Col 283-288; 206pp; English.

XX

CC The invention relates to a combination comprising a number of  
 CC substantially purified and isolated polynucleotides which are co-  
 CC expressed with genes known to be involved in bone remodelling and  
 CC osteoporosis. The invention is used to diagnose disorders associated with  
 CC bone remodelling or osteoporosis. ABS70344-ABS70512 represent human bone  
 CC remodelling genes of the invention

XX

SQ Sequence 4822 BP; 1441 A; 1046 C; 1073 G; 1247 T; 0 U; 15 Other;

Query Match 62.1%; Score 2323.8; DB 6; Length 4822;  
 Best Local Similarity 80.9%; Pred. No. 0;  
 Matches 3060; Conservative 0; Mismatches 587; Indels 137; Gaps 25;

Qy 63 CGCGAAGGCAGCAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTTCG 122  
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 Db 78 CNCGGAGGCAGGAGGAGCAGTCTCATTGTTCCGGGAGCCGTCACCACAGTAGGTCCCTCG 137

Qy	123	GCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACAAC	182
Db	138	GCTCAGT-----CGGCCAGCCCCCTCTCAGTCCTCCCCAACCCCCACAAC	182
Qy	183	CGCCCGCGACTCTGAGGAGAAGCGGC-CCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCG	241
Db	183	CGCCCGCGGCTCTGAGACGCGGCCCCGGNGGCGGCGGCAGCAGCTGCAGCATCATC-TCC	241
Qy	242	ACCCGCCAGCCATGGAAGACATAGACCAGTCGTGCTGGTCTCCTCGTCCACGGACAGCC	301
Db	242	ACCTTCAGCCATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCTCGGACAGCC	298
Qy	302	CGCCCCGGCCTCCGCCCCGCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGG	361
Db	299	CACCCCGGCCGCGAGCCCGCTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG-	357
Qy	362	ACGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGC	421
Db	358	--GAAGAAGAGGANGATGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGC	415
Qy	422	TGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCGAGCTGCGGTGC-----CGCCCGCCGCCG	475
Db	416	TGGAGAGGAAGCCCGCCGCGGGCTGTCCGCGGCCCCAGTGCCACCGCCCTGCCGCCG	475
Qy	476	CCGCGCCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGC	535
Db	476	GCGGCCCNNTAATGGACTTCGGAATGACTTCGTGCCGCGGCGCCCCGGGGACCCCTGC	535
Qy	536	CGGCCGCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----	589
Db	536	CGGCCGCTCCCCCGCTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCTGT	595
Qy	590	---CGGCGCCCGCGCCATCCCTGCCGCCCCGCTGCCGCAGTCTTGCCCTCCAAGCTCCCAG	646
Db	596	CGACCGTGCCCGCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTG	655
Qy	647	AGGACGACGAGCCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGG	706
Db	656	AGGACGACGAGCCTCCGGCCCCGGCCTCCCCCTCCTCCCCCGGCCAGCGTGAGCCCCCAGG	715
Qy	707	CGGAGC-----CCGCCGCGCCCCCTTCCACGCCGGCCG	739
Db	716	CAGAGCCCGTGTGGANCCCGCCAGCCCCGGCTNCCGCCGCGCCCCCTCCACCCGGCCG	775
Qy	740	CGCCCAAGCGCAGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTG	796
Db	776	CGCCCAAGCGCAGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTG	835
Qy	797	CATCTGAGCCTGTGATAACCTCCTCTGCAGAAAAATTATGGATTTGATGGAGCAGCCAG	856
Db	836	CATCTGAGCCTGTGATACGCTCCTCTGCAGAAAA--TATGGACTTGAAGGAGCAGCCAG	892
Qy	857	GTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCCT	916
Db	893	GTAACACTATTTTCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCTT	952



Qy 917 CTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTA 976  
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 Db 953 CTCTTCCTTCTCTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTA 1012

Qy 977 ACTTATCAGCAGTGTCTCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTA 1036  
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 Db 1013 ATTTGTCAACAGTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTA 1072

Qy 1037 AAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAAATTTTCAG 1096  
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 Db 1073 AAGAGGTCTCAGAGAAGGCAAAAACCTCTACTCATAGATAGAGATTTAACAGAGTTTTCAG 1132

Qy 1097 AATTAGAATATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCA 1156  
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 Db 1133 AATTAGAATACTCAGAAATGGGATCATCGTTAGTGTCTCTCCAAAAGCAGAAATCTGCCG 1192

Qy 1157 TATTAGTAGAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATT 1213  
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 Db 1193 TAATAGTAGCAAATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGT 1252

Qy 1214 TAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGG 1258  
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 Db 1253 TAGTTAGTAATAACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGG 1312

Qy 1259 GTAAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGA 1318  
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 Db 1313 TTAAAGAGGATGAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTAAATGAAAGAGAG 1372

Qy 1319 TGTCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCAT 1378  
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 Db 1373 TTGCAGTGGAAGCTCCTATGAGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTAT 1432

Qy 1379 GGAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT----- 1431  
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 Db 1433 GGAAGTGAAAGATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAATCG 1489

Qy 1432 -----AATGTGGAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAA 1486  
 |||||  
 Db 1490 AGAGCAACTTGGAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACTA 1549

Qy 1487 GTCTTGGAAGGATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAAC 1546  
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 Db 1550 ATCACGAAAAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAG 1609

Qy 1547 CTGTGAAGGACAGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCG 1603  
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 Db 1610 GTATAAAGGATCGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTG 1669

Qy 1604 AAAGCACCACAGCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAACAG 1663  
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 Db 1670 AGAGCATTGCAACAAACATTTTCCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCG 1729

Qy 1664 ATG-AAAAAAAAATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCC 1719  
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 Db 1730 ATGAAAAAAAAAATAGAAGAAAGGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACC 1789

Qy 1720 AAAACGTCAAATCC-TTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAAC 1778

Db	1790	AAAAACATCAAACCCTTTTACTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAAC	1849
Qy	1779	AGATACCTTATCAAAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCC	1838
Db	1850	AGATAATTTAACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCC	1909
Qy	1839	AGATTTAGTTTCAGGAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGC	1898
Db	1910	AGATTTAGTACAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGC	1969
Qy	1899	TTATGAAACAAAAGTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCC	1958
Db	1970	TTATGAAACAAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCC	2029
Qy	1959	CACAGCACAGCTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTGGCC	2018
Db	2030	TGCAGCACAGCTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTGGCC	2089
Qy	2019	TGATATTGTTATGGAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGT	2078
Db	2090	TGACATTGTTATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGAT	2149
Qy	2079	GCAGCCCAGTGTATCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCT	2138
Db	2150	ACAGCCCAGCTCATCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACA	2206
Qy	2139	TGAGCCTGAAAACCCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTT	2195
Db	2207	TGAGCCTGAAAACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATC	2266
Qy	2196	GGGAACAAAGGAAGGAATAAAAGAGCCTGAAAGTTTAAATGCAGCTGTTTCAGGAAACAGA	2255
Db	2267	AGGAATAAAGGAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGA	2326
Qy	2256	AGCTCCTTATATATCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCC	2315
Db	2327	AGCTCCTTATATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACC	2386
Qy	2316	AAGTCCAGATTTCTCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACA	2375
Db	2387	AGCTCCGGATTTCTCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCA	2446
Qy	2376	CGCTGAGCTAGTGGAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGA	2435
Db	2447	TTCTGAGCTAGTTGAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGA	2506
Qy	2436	TTCGATTCTGAAGTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCT	2495
Db	2507	TTCAATACCTGACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCT	2566
Qy	2496	CACTGA-----AGTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTC	2549
Db	2567	CACTGAGACTTCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTT	2626
Qy	2550	ACCTCAGGAGCTAGGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAA	2609

Db 2627 GCCACCTGAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAA 2686  
 Qy 2610 AGATGC---TGCATCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCA 2666  
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 Db 2687 AGATACCTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCA 2746  
 Qy 2667 AATGGAAGAGTTTAATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGA 2726  
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 Db 2747 GATGGAGGAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGC 2806  
 Qy 2727 CAAAATAAAAGAAAGTGAAACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATT 2786  
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 Db 2807 ACAGATAAGAGAAACTGAAACGTTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTT 2866  
 Qy 2787 TCCCACGTTTGTCAGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGA 2843  
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 Db 2867 CCCTACATTGATCAGTTCTAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGA 2926  
 Qy 2844 TCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCC 2903  
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 Db 2927 CCTAGAAGTATCCACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCTATTGCC 2986  
 Qy 2904 TTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG---- 2959  
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 Db 2987 TTGCACAGAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAA 3046  
 Qy 2960 --TACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATC 3017  
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 Db 3047 AATCAGTTTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATT 3106  
 Qy 3018 GCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAA 3077  
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 Db 3107 GCCTCCAGATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAA 3166  
 Qy 3078 ATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATC 3137  
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 Db 3167 AGTTCTTGTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATC 3226  
 Qy 3138 CCTGTCAGCTGTATTGTCAGCAGAGCTGAG-TAAAACCTTCAGTTGTTGACCTCCTCTACT 3196  
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 Db 3227 ACCATCTGCTATATTTTCAGCAGAGCTGAGCTAAAACCTTCAGTTGTTGACCTCCTGTACT 3286  
 Qy 3197 GGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTC 3256  
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 Db 3287 GGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCTGCTGCTTTTCAT 3346  
 Qy 3257 TGACAGTGTTTCAGCATTGTGAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGA 3316  
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 Db 3347 TGACAGTATTTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGA 3406  
 Qy 3317 CTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCC 3376  
 | |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||  
 Db 3407 CCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCC 3466  
 Qy 3377 ACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAAT 3436  
 |||| |||| |||| || |||| |||| |||| |||| |||| |||| |||| |||| || ||||  
 Db 3467 ACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGT 3526

Qy 3437 ACAGTAATTCTGCTCTTGGTCATGTGAACAGCACATAAAAGAACTGAGGCGGCTTTTCT 3496  
 |||  
 Db 3527 ACAGTAATTCTGCTCTTGGTCATGTGAACAGCACATAAAAGGAACTCAGGCGCCTCTTCT 3586  
 Qy 3497 TAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATG 3556  
 |||  
 Db 3587 TAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTACCTATG 3646  
 Qy 3557 TTGGTGCCTTGTTCATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTA 3616  
 |||  
 Db 3647 TTGGTGCCTTGTTCATGGTCTGACACTACTGATTTTAGCTCTCATTTCACTCTTCAGTG 3706  
 Qy 3617 TTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACA 3676  
 |||  
 Db 3707 TTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATA 3766  
 Qy 3677 AGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG 3736  
 |||  
 Db 3767 AGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG 3826  
 Qy 3737 CAGA 3740  
 |||  
 Db 3827 CTGA 3830

RESULT 8

ABX34563

ID ABX34563 standard; cDNA; 4698 BP.

XX

AC ABX34563;

XX

DT 13-FEB-2003 (first entry)

XX

DE Human mddt cDNA SEQ ID 124.

XX

KW MDDT; human; disease detection and treatment molecule polypeptide;  
 KW anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;  
 KW haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;  
 KW gene therapy; protein replacement therapy; cell proliferative disorder;  
 KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;  
 KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;  
 KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;  
 KW psoriasis; hepatitis; gene; ss.

XX

OS Homo sapiens.

XX

PN WO200279449-A2.

XX

PD 10-OCT-2002.

XX

PF 27-MAR-2002; 2002WO-US009944.

XX

PR 28-MAR-2001; 2001US-0279619P.

PR 29-MAR-2001; 2001US-0280067P.

PR 29-MAR-2001; 2001US-0280068P.

PR 16-MAY-2001; 2001US-0291280P.

PR 17-MAY-2001; 2001US-0291829P.  
PR 17-MAY-2001; 2001US-0291849P.  
PR 19-JUN-2001; 2001US-0299428P.  
PR 20-JUN-2001; 2001US-0299776P.  
PR 20-JUN-2001; 2001US-0300001P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;  
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;  
PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;  
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;  
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;

XX

DR WPI; 2003-058431/05.

DR P-PSDB; ABU11573.

XX

PT New purified disease detection and treatment molecule proteins and  
PT polynucleotides, useful for diagnosing, treating or preventing cancers  
PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis  
PT or hepatitis.

XX

PS Claim 1; SEQ ID NO 124; 339pp + Sequence Listing; English.

XX

CC This invention describes a novel disease detection and treatment molecule  
CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,  
CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,  
CC antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides  
CC and the polypeptides of the invention can be used for gene therapy,  
CC protein replacement therapy and are useful for treating a variety of  
CC diseases or conditions. These polypeptides or polynucleotides are  
CC particularly useful for diagnosing, treating or preventing cell  
CC proliferative disorders (e.g. cancers including adenocarcinoma,  
CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's  
CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's  
CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or  
CC hepatitis. ABX34440-ABX34835 encode the MDDT polypeptides represented in  
CC ABU11450-ABU11845, described in the disclosure of the invention. NOTE:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 4698 BP; 1410 A; 1028 C; 1022 G; 1238 T; 0 U; 0 Other;

Query Match 61.4%; Score 2297.4; DB 7; Length 4698;  
Best Local Similarity 80.7%; Pred. No. 0;  
Matches 2996; Conservative 0; Mismatches 596; Indels 121; Gaps 22;

Qy 134 CACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCCAACCCCCACAACCGCCCGCGACT 193  
| || ||| | | ||| ||||| ||||| | ||||| ||||| |||||  
Db 23 CTCGGCTCAGTCGGCCCAGCCCCTCTCAGTCCTCCCCAACCCCCACAACCGCCCGCGCTC 82  
  
Qy 194 CTGAGGAGAAGCGGCCCTGCGGGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCCA 253  
||||| | | | ||||| | ||||| || || ||||| |||||  
Db 83 CTGAGACGCGCCCCGGCGGGCGGGCAGCAGCTGCAGCATCATC-TCCACCCTCCAGCCA 141  
  
Qy 254 TGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCGGCCTC 313

Accession	Position	Sequence	Length
Db	142	TGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCTCGGACAGCCCACCCCGGCCGC	198
Qy	314	CGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAGG	373
Db	199	AGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAGG	255
Qy	374	AGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAGC	433
Db	256	AGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAGC	315
Qy	434	CCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCGCCGCCGCCGCCGCCGCTGC	487
Db	316	CCGCCGCCGGGCTGTCCGCAGGCCCCAGTGCCCCACCGCCCCTGCCGCCGGCGGCCCTTGA	375
Qy	488	TGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCCGGGGCCGCTGCCGGCCGCGCCCC	547
Db	376	TGGACTTCGGAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTTCCC	435
Qy	548	CTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCCG	598
Db	436	CCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCTCGACCGTGCCCG	495
Qy	599	CGCCATCCCTGCCGCCCCTGCCGCAGTCTGCCCTCCAAGCTCCCAGAGGACGACGAGC	658
Db	496	CGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAGC	555
Qy	659	CTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG-----	711
Db	556	CTCCGGCCCGGCTCCCCCTCCTCCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTGT	615
Qy	712	-----CCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGCA	751
Db	616	GGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCGCGCCGCGCCCAAGCGCA	675
Qy	752	GGGGCTCC---GGCTCAGTGGATGAGACCC--TTTTTGCTCTTCTGCTGCATCTGAGC	805
Db	676	GGGGCTCCTCGGGCTCAGATGGATGAGACCCATTTTTGCTCTTACCTGCTGCATCTGAGC	735
Qy	806	CTGTGATACCCTCCTCTGCAGAAAAATTTATGGATTTGATGGAGCAGCCAGGTAACACTG	865
Db	736	CTGTGATACGCTCCTC--ATGCAGAAATATGGACTTGAAGGAGCAGCCAGGTAACACTA	793
Qy	866	TTTCGTCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAAACTGCTGCCTCTCTTCCTT	925
Db	794	TTTCGGCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAAACTGCTGCTTCTCTTCCTT	853
Qy	926	CTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACCTATCAG	985
Db	854	CTCTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAA	913
Qy	986	CAGTGTCTATCCTCAGAAGGAACAATTGAAG-AACTTTAAATGAAGCTTCTAAAGAGTTG	1044
Db	914	CAGTATTACCCACTGAAGGAACACTTCAAGAAAAATGTCAGTGAAGCTTCTAAAGAGGTC	973
Qy	1045	CCAGAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAA	1104

Db 974 TCAGAGAAGGCCAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAA 1033  
 Qy 1105 TATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTA 1164  
 || ||||| ||||| || | | ||| ||||| ||| || ||| || |||||  
 Db 1034 TACTCAGAAATGGGATCATCGTTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTA 1093  
 Qy 1165 GAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGT 1221  
 | ||| ||| ||||| ||||| |||| | |||| | | ||||| ||  
 Db 1094 GCAAATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGT 1153  
 Qy 1222 AGTGCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAA 1266  
 | | ||||| | || ||||| | |||| ||| |||||  
 Db 1154 AATAACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAG 1213  
 Qy 1267 GACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTA 1326  
 || ||||| ||||| ||||| ||| ||||| ||||| || | |||||  
 Db 1214 GATGAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTG 1273  
 Qy 1327 GTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTG 1386  
 | ||| ||| ||||| || ||||| ||||| ||||| ||| ||||| |||||  
 Db 1274 GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1333  
 Qy 1387 AAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AAT 1434  
 ||||| | ||| | ||| ||| || ||||| |||| | ||  
 Db 1334 AAAGATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAATCGAGAGCAAC 1390  
 Qy 1435 GTGGAAAGTAAAGTGGACAGAAAATGCTTGAAGATAGCCTGGAGCAAAAAAGTCTTGGG 1494  
 ||||| ||||| || ||||| || ||||| ||||| ||||| || |||  
 Db 1391 TTGGAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACTAATCACGAA 1450  
 Qy 1495 AAGGATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAG 1554  
 || ||||| || ||||| || ||||| ||||| ||||| ||||| || |||  
 Db 1451 AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAG 1510  
 Qy 1555 GACAGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACC 1611  
 || | || ||||| || ||||| ||||| ||||| ||||| || |||||  
 Db 1511 GATCGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATT 1570  
 Qy 1612 ACAGCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAA 1671  
 || ||||| || ||||| ||||| ||||| ||||| ||||| || |||||  
 Db 1571 GCAACAAACATTTTCCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA 1630  
 Qy 1672 AAAATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCA 1728  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1631 AAAATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCA 1690  
 Qy 1729 AATCCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTA 1788  
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||  
 Db 1691 AACCCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTA 1750  
 Qy 1789 TCAAAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTT 1848  
 ||||| ||||| || ||||| ||||| ||||| ||||| |||||  
 Db 1751 ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA 1810  
 Qy 1849 CAGGAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACA 1908  
 ||||| ||||| ||||| ||||| || ||||| ||||| |||||  
 Db 1811 CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA 1870

Qy	1909	AAAGTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAG	1968
Db	1871	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1930
Qy	1969	CTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCAACAGTTTTCCTGATATTGTT	2028
Db	1931	CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACAGTTTTCCTGACATTGTT	1990
Qy	2029	ATGGAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGT	2088
Db	1991	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	2050
Qy	2089	GTATCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAA	2148
Db	2051	TCATCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA	2107
Qy	2149	AACCCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAG	2205
Db	2108	AACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2167
Qy	2206	GAAGGAATAAAAGAGCCTGAAAGTTTAAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTAT	2265
Db	2168	GAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2227
Qy	2266	ATATCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGAT	2325
Db	2228	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTCTGCTGAACCAGCTCCGGAT	2287
Qy	2326	TTCTCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTA	2385
Db	2288	TTCTCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTA	2347
Qy	2386	GTGGAGGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTGATTCCCT	2445
Db	2348	GTTGAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCT	2407
Qy	2446	GAAGTCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA----	2501
Db	2408	GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2467
Qy	2502	--AGTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAG	2559
Db	2468	TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAG	2527
Qy	2560	CTAGGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---T	2616
Db	2528	GGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCTTG	2587
Qy	2617	GCATCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAG	2676
Db	2588	TTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAG	2647
Qy	2677	TTTAATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAA	2736
Db	2648	CTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGA	2707



Qy	2737	GAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTT	2796
Db	2708		
Qy	2797	GAACTGAAACGTTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCTACATTG	2767
Qy	2797	GTCAGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTA	2853
Db	2768		
Qy	2797	ATCAGTTCTAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTA	2827
Qy	2854	TCCGACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAA	2913
Db	2828		
Qy	2854	TCCCACAAAAGTGAAATTGCTAATGCCCCGATGGAGCTGGGTTCATTGCCTTGACAGAA	2887
Qy	2914	TTGCCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTT	2967
Db	2888		
Qy	2914	TTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTC	2947
Qy	2968	TCAGATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAAT	3027
Db	2948		
Qy	2968	TCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGAT	3007
Qy	3028	GTCTCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACG	3087
Db	3008		
Qy	3028	GTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTG	3067
Qy	3088	AAAGAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCT	3147
Db	3068		
Qy	3088	AAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCT	3127
Qy	3148	GTATTGTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATT	3207
Db	3128		
Qy	3148	ATATTTTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATT	3187
Qy	3208	AAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTT	3267
Db	3188		
Qy	3208	AAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTTTTATTGACAGTATTC	3247
Qy	3268	AGCATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTT	3327
Db	3248		
Qy	3268	AGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTT	3307
Qy	3328	AGGATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGG	3387
Db	3308		
Qy	3328	AGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGG	3367
Qy	3388	GCATATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTTCAGAAATACAGTAATTCT	3447
Db	3368		
Qy	3388	GCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAATACAGTAATTCT	3427
Qy	3448	GCTCTTGGTCATGTGAACAGCACAATAAAGAACTGAGGCGGCTTTTCTTAGTTGATGAT	3507
Db	3428		
Qy	3448	GCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGAT	3487
Qy	3508	TTAGTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTG	3567
Db	3488		
Qy	3508	TTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTG	3547
Qy	3568	TTCAATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATT	3627

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      || |||||
Db      3548 TTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTTCCTGTTATT 3607
      |||||
Qy      3628 TATGAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAG 3687
      |||||
Db      3608 TATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAA 3667
      |||||
Qy      3688 GATGCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
      |||||
Db      3668 GATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3720

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RESULT 9

AAZ56886

ID AAZ56886 standard; DNA; 3579 BP.

XX

AC AAZ56886;

XX

DT 25-APR-2000 (first entry)

XX

DE Human MAGI polypeptide encoding DNA.

XX

KW MAGI protein; neuroendocrine-specific protein; neuropathy; human;  
 KW spinal injury; neuronal degeneration; neuromuscular disorder; cancer;  
 KW psychiatric disorder; developmental disorder; inflammatory disorder;  
 KW stroke; cytostatic; cerebroprotective; neuroprotective; ds.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	CDS	1. .3579
FT		/*tag= a
FT		/product= "MAGI polypeptide"

XX

PN WO200005364-A1.

XX

PD 03-FEB-2000.

XX

PF 21-JUL-1999; 99WO-GB002360.

XX

PR 22-JUL-1998; 98GB-00016024.

PR 19-JUL-1999; 99GB-00016898.

XX

PA (SMIK ) SMITHKLINE BEECHAM PLC.

XX

PI Michalovich D, Prinjha RK;

XX

DR WPI; 2000-182693/16.

DR P-PSDB; AAY56967.

XX

PT Novel polypeptides related to neuroendocrine-specific proteins and  
 PT polynucleotides useful for diagnosis of various diseases and for  
 PT treatment of cancer and neurological disorders.

XX

PS Claim 5; Page 19-20; 35pp; English.

XX

CC The invention relates to human MAGI protein, which is similar to

neuroendocrine-specific protein. The MAGI protein can be expressed by standard recombinant methodology. The MAGI polypeptides, polynucleotides and antibodies are useful for treating diseases, including neuropathies, spinal injury, neuronal degeneration, neuromuscular disorders, psychiatric disorders and developmental disorders, cancer, stroke and inflammatory disorders. The polynucleotide is also useful for chromosome localization and for tissue expression studies. The present sequence represents a DNA encoding the human MAGI protein

SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;

Query Match 61.2%; Score 2289.2; DB 3; Length 3579;  
Best Local Similarity 81.5%; Pred. No. 0;  
Matches 2925; Conservative 0; Mismatches 548; Indels 117; Gaps 19;

Qy	253	ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCT	312
Db	1	ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCCTCGGACAGCCCACCCCGGCCG	57
Qy	313	CCGCCCCGCTTCAAGTACCAGTTTCGTGACGGAGCCCCGAGGACGAGGAGGACGAGGAGGAG	372
Db	58	CAGCCCCGCTTCAAGTACCAGTTTCGTGAGGGAGCCCCGAGGACGAGGAG---GAAGAAGAG	114
Qy	373	GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAAGTGGAGGTGCTGGAGAGGAAG	432
Db	115	GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG	174
Qy	433	CCCGCAGCCGGGGCTGTCCGCAGCTGCGGTGC-----CGCCCGCCGCCCGCCGCGCCGCTG	486
Db	175	CCCGCCCGCCGGGGCTGTCCGCGGCCCCAGTGCCACCGCCCCCTGCCGCCGGCGCGCCCTG	234
Qy	487	CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCCGGGGCCGCTGCCGGCCGCGCCCC	546
Db	235	ATGGACTTCGGAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC	294
Qy	547	CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC	597
Db	295	CCCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTCGACCGTGCCC	354
Qy	598	GCGCCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAG	657
Db	355	GCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG	414
Qy	658	CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG-----	711
Db	415	CCTCCGGCCCCGGCCTCCCCCTCCTCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG	474
Qy	712	-----CCCCGCCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC	750
Db	475	TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCGGCCGCGCCCAAGCGC	534
Qy	751	AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT	807
Db	535	AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT	594
Qy	808	GTGATACCCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT	867

Db	595	GTGATACGCTCCTCTGCAGAAAA--TATGGACTTGAAGGAGCAGCCAGGTAACACTATT	651
Qy	868	TCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAACTGCTGCCTCTCTTCCTTCT	927
Db	652	TCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAACTGCTGCTTCTCTTCCTTCT	711
Qy	928	CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA	987
Db	712	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAAATTTGTCAACA	771
Qy	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Db	772	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	831
Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Db	832	GAGAAGGCAAAACCTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC	891
Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Db	892	TCAGAAATGGGATCATCGTTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	951
Qy	1168	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT	1224
Db	952	AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1011
Qy	1225	GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC	1269
Db	1012	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1071
Qy	1270	AGAGTTGTGTCTCCAGAAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA	1329
Db	1072	GAAGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGAA	1131
Qy	1330	GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA	1389
Db	1132	GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA	1191
Qy	1390	GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG	1437
Db	1192	GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG	1248
Qy	1438	GAAAGTAAAGTGGAACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAGTCTTGGAAG	1497
Db	1249	GAAAGTAAAGTGGAATAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAAAAA	1308
Qy	1498	GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC	1557
Db	1309	GATAGTGAAGGATAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAGGTATAAAGGAT	1368
Qy	1558	AGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCT---CAGCAACCGAAAGCACCACA	1614
Db	1369	CGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATTGCA	1428
Qy	1615	GCAAACACTTTCCCTTTGTTAGAAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA	1674
Db	1429	ACAAACATTTTCCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAA	1488

Qy	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT	1731
Db	1489	ATAGAAGAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAAC	1548
Qy	1732	CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Db	1549	CCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA	1608
Qy	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG	1851
Db	1609	AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG	1668
Qy	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Db	1669	GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA	1728
Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Db	1729	ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT	1788
Qy	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	2031
Db	1789	TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG	1848
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA	2091
Db	1849	GAAGCACCATTGAATTCTGCAGTTCCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA	1908
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Db	1909	TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	1965
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	1966	CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA	2025
Qy	2209	GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268
Db	2026	GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA	2085
Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC	2328
Db	2086	TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTTC	2145
Qy	2329	TCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Db	2146	TCTGATTATTTCAGAAATGGCAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2205
Qy	2389	GAGGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCTGAA	2448
Db	2206	GAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2265
Qy	2449	GTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2266	GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2325

Qy 2503 GTGTCTGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA 2562  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 2326 TTTGAGTCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCTTTGCCACCTGAGGGA 2385

Qy 2563 GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA 2619  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 2386 GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA 2445

Qy 2620 TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTT 2679  
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 Db 2446 CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTC 2505

Qy 2680 AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA 2739  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 2506 AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA 2565

Qy 2740 AGTGAAACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC 2799  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 2566 ACTGAAACGTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTTCCTACATTGATC 2625

Qy 2800 AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC 2856  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 2626 AGTTCTAAACTGATTCAATTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC 2685

Qy 2857 GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCAATGCCTTGCTTAGAATTG 2916  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 2686 CACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCAATGCCTTGACAGAATTG 2745

Qy 2917 CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA 2970  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 2746 CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA 2805

Qy 2971 GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC 3030  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 2806 GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT 2865

Qy 3031 TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA 3090  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 2866 TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA 2925

Qy 3091 GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA 3150  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 2926 GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA 2985

Qy 3151 TTGTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG 3210  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 2986 TTTTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG 3045

Qy 3211 AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTACGC 3270  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 3046 AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTTATTGACAGTATTCAGC 3105

Qy 3271 ATTGTGAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG 3330  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 3106 ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG 3165

Qy 3331 ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA 3390



PI Michalovich D, Prinjha R;

XX

DR WPI; 2001-343822/36.

DR P-PSDB; AAB82349.

XX

PT New polypeptide designated NOGO-C is a splice variant of the human NOGO  
PT gene and may be useful in the treatment of neural disorders including  
PT Alzheimer's and Parkinson's diseases.

XX

PS Disclosure; Page 25-26; 25pp; English.

XX

CC The present sequence is that of cDNA encoding human NOGO-A (see  
CC AAB82349). NOGO-A is a previously known splice variant of the human NOGO  
CC gene on chromosome 2p21. NOGO-A cDNA was obtained by PCR amplification of  
CC human spinal cord cDNA. The invention relates to a novel splice variant,  
CC NOGO-C (see AAF90323). It provides NOGO-C polypeptides and  
CC polynucleotides, and methods for producing such polypeptides by  
CC recombinant techniques. Also disclosed are methods for utilising NOGO-C  
CC polypeptides and polynucleotides in the treatment of diseases including  
CC neuropathies, spinal injury, brain injury, stroke, neuronal degeneration,  
CC for example Alzheimer's disease and Parkinson's disease, neuromuscular  
CC disorders, psychiatric disorders and developmental disorders. Also  
CC provided are methods for identifying agonists and agonists for use in  
CC treating conditions associated with NOGO-C imbalance, and diagnostic  
CC assays for detecting diseases associated with inappropriate NOGO-C  
CC activity or levels

XX

SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;

Query Match 61.2%; Score 2289.2; DB 4; Length 3579;

Best Local Similarity 81.5%; Pred. No. 0;

Matches 2925; Conservative 0; Mismatches 548; Indels 117; Gaps 19;

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Qy      253 ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCT 312
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1  ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCCTCGGACAGCCACCCCGGCCG 57

Qy      313 CCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG 372
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      58  CAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 114

Qy      373 GAGGAGGACGAGGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG 432
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      115 GAGGAGGAAGAGGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG 174

Qy      433 CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCGCCGCGCCGCGCCGCTG 486
          |||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      175 CCCGCCGCGGGCTGTCCGCGGCCCCAGTGCCACCGCCCTGCCGCCGGCGCGCCCTG 234

Qy      487 CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCCGGGCCGCTGCCGGCCGCGCCC 546
          ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db      235 ATGGACTTCGGAATGACTTCGTGCCGCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC 294

Qy      547 CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC 597
          || | || | | | | | | | | | | | | | | | | | | | | | | |
Db      295 CCCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTCGACCGTGCCC 354
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Qy	598	GCGCCATCCCTGCCGCCCGCTGCCCGAGTCTTGCCTCCAAGCTCCCAGAGGACGACGAG	657
Db	355	GCGCCATCCCCGCTGTCTGCTGCCGCGAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG	414
Qy	658	CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG-----	711
Db	415	CCTCCGGCCCCGGCCTCCCCCTCCTCCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG	474
Qy	712	-----CCCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC	750
Db	475	TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCCGCCGCGCCCAAGCGC	534
Qy	751	AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT	807
Db	535	AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT	594
Qy	808	GTGATACCCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT	867
Db	595	GTGATACGCTCCTCTGCAGAAA--TATGGACTTGAAGGAGCAGCCAGGTAACACTATT	651
Qy	868	TCGTCTGGTCAAGAGGATTTCCCATCTGTCTTGCTTGAAGTCTGCCTCTCTTCCTTCT	927
Db	652	TCGGCTGGTCAAGAGGATTTCCCATCTGTCTTGCTTGAAGTCTGCCTCTCTTCCTTCT	711
Qy	928	CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA	987
Db	712	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	771
Qy	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Db	772	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	831
Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Db	832	GAGAAGGCAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC	891
Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Db	892	TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	951
Qy	1168	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT	1224
Db	952	AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1011
Qy	1225	GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC	1269
Db	1012	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1071
Qy	1270	AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTAATGAAATGCAGATGTCAGTAGTA	1329
Db	1072	GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGAA	1131
Qy	1330	GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA	1389
Db	1132	GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA	1191
Qy	1390	GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG	1437

Db	1192	GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG	1248
Qy	1438	GAAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAGTCTTGGAAG	1497
Db	1249	GAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAAAAA	1308
Qy	1498	GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGAC	1557
Db	1309	GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT	1368
Qy	1558	AGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCT---CAGCAACCGAAAGCACCACA	1614
Db	1369	CGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA	1428
Qy	1615	GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAA	1674
Db	1429	ACAAACATTTTCCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAAA	1488
Qy	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT	1731
Db	1489	ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAAC	1548
Qy	1732	CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Db	1549	CCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA	1608
Qy	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG	1851
Db	1609	AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG	1668
Qy	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Db	1669	GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA	1728
Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCCACAGCACAGCTT	1971
Db	1729	ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT	1788
Qy	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCAACAGTTTTGCCTGATATTGTTATG	2031
Db	1789	TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAAGTTTTGCCTGACATTGTTATG	1848
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA	2091
Db	1849	GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA	1908
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Db	1909	TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	1965
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	1966	CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA	2025
Qy	2209	GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268

Db 2026 GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA 2085

Qy 2269 TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC 2328  
 || ||||| ||||| ||||| ||||| || ||||| ||| |||||

Db 2086 TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTTC 2145

Qy 2329 TCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG 2388  
 ||| ||||| ||||| ||||| || || || ||||| || || |||||

Db 2146 TCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT 2205

Qy 2389 GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTGATTTCCTGAA 2448  
 || ||||| ||||| ||||| ||||| ||||| ||||| || |||||

Db 2206 GAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC 2265

Qy 2449 GTCCCAACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A 2502  
 || ||||| ||||| || ||||| ||||| ||||| ||||| |||||

Db 2266 GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA 2325

Qy 2503 GTGTCTGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA 2562  
 | | ||| | ||| ||||| ||||| ||||| ||||| |||||

Db 2326 TTTGAGTCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCTTTGCCACCTGAGGGA 2385

Qy 2563 GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA 2619  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2386 GGAAAGCCATATTTGGAATCTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA 2445

Qy 2620 TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTT 2679  
 || ||||| || ||||| ||||| ||||| ||||| ||||| |||||

Db 2446 CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAGCTC 2505

Qy 2680 AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA 2739  
 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2506 AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA 2565

Qy 2740 AGTGAAACATTTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC 2799  
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Db 2566 ACTGAAACGTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATC 2625

Qy 2800 AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC 2856  
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Db 2626 AGTTCTAAAACTGATTCAATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC 2685

Qy 2857 GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCAATGCCTTGCTTAGAATTG 2916  
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Db 2686 CACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCAATGCCTTGACAGAATTG 2745

Qy 2917 CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA 2970  
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Db 2746 CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA 2805

Qy 2971 GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC 3030  
 ||||| || || ||||| ||||| | ||||| ||||| ||||| |||||

Db 2806 GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT 2865

Qy 3031 TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA 3090  
 ||||| ||||| ||||| ||| ||||| ||||| ||||| |||||

Db 2866 TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA 2925



KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;  
 KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;  
 KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;  
 KW tissue hypertrophy; central nervous system; axon regeneration; NogoA;  
 KW Nogo-associated disease; metastasis; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1. .3579  
 FT /\*tag= a  
 FT /product= "Human NogoA protein"  
 XX  
 PN WO200257483-A2.  
 XX  
 PD 25-JUL-2002.  
 XX  
 PF 18-JAN-2002; 2002WO-GB000228.  
 XX  
 PR 18-JAN-2001; 2001GB-00001312.  
 XX  
 PA (GLAX ) GLAXO GROUP LTD.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 PI Blackstock WP, Hale RS, Prinjha R, Rowley A;  
 XX  
 DR WPI; 2002-599722/64.  
 DR P-PSDB; ABG30938.  
 XX  
 PT Identifying modulators of Nogo or BACE activity for treating acute  
 PT neuronal injuries, neoplastic or dysproliferative disorders, comprises  
 PT providing and monitoring interaction between Nogo and BACE polypeptides.  
 XX  
 PS Disclosure; Page 53-58; 68pp; English.  
 XX  
 CC The present invention relates to a new method of identifying modulators  
 CC of Nogo function or BACE activity. The method involves providing Nogo and  
 CC BACE polypeptides capable of binding with each other, monitoring the  
 CC interaction between these polypeptides, and determining if the test agent  
 CC is a modulator of Nogo or BACE activity. The method is useful in treating  
 CC acute neuronal injuries, such as spinal or head injury, stroke,  
 CC peripheral nerve damage, and in neoplastic (e.g. glioblastomas,  
 CC neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.  
 CC cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue  
 CC hypertrophy) of the central nervous system. The BACE polypeptide is  
 CC useful in screening methods to identify agents that may act as modulators  
 CC of BACE activity and in particular agents that may be useful in treating  
 CC Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,  
 CC and the polynucleotide encoding the BACE polypeptide are useful in  
 CC manufacturing a medicament for the treatment or prevention of disorders  
 CC responsive to the modulation of Nogo activity, in alleviating the  
 CC symptoms or improving the condition of a patient suffering from this  
 CC disorder, in axon regeneration, or in preventing metastasis or spreading  
 CC of a cancer. The polynucleotide may also be an essential component in  
 CC assays, a probe, in recombinant protein synthesis, and in gene therapy  
 CC techniques. The present nucleic acid sequence encodes the human NogoA  
 CC protein of the invention

SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;

Query Match 61.2%; Score 2289.2; DB 6; Length 3579;  
Best Local Similarity 81.5%; Pred. No. 0;  
Matches 2925; Conservative 0; Mismatches 548; Indels 117; Gaps 19;

[illegible]

Db	712	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAAATTTGTCAACA	771
Qy	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Db	772	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	831
Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Db	832	GAGAAGGCAAAAACCTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC	891
Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Db	892	TCAGAAATGGGATCATCGTTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	951
Qy	1168	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT	1224
Db	952	AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1011
Qy	1225	GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC	1269
Db	1012	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1071
Qy	1270	AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA	1329
Db	1072	GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTTAAATGAAAAGAGAGTTGCAGTGGAA	1131
Qy	1330	GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA	1389
Db	1132	GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA	1191
Qy	1390	GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG	1437
Db	1192	GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG	1248
Qy	1438	GAAAGTAAAGTGGACAGAAAATGCTTGGAGATAGCCTGGAGCAAAAAAGTCTTGGAAG	1497
Db	1249	GAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAAAAA	1308
Qy	1498	GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCAGTACCCCAGAACCTGTGAAGGAC	1557
Db	1309	GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCAGTACGCCAGAAGGTATAAAGGAT	1368
Qy	1558	AGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCT---CAGCAACCGAAAGCACCACA	1614
Db	1369	CGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA	1428
Qy	1615	GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA	1674
Db	1429	ACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAA	1488
Qy	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT	1731
Db	1489	ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAAC	1548
Qy	1732	CCTTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Db	1549	CCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA	1608

Qy	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTTCAG	1851
Db	1609	AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG	1668
Qy	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Db	1669	GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA	1728
Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Db	1729	ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT	1788
Qy	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	2031
Db	1789	TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG	1848
Qy	2032	GAAGCACCATTAAATTCTCTCTCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA	2091
Db	1849	GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA	1908
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Db	1909	TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	1965
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGAACAAAGGAA	2208
Db	1966	CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA	2025
Qy	2209	GGAATAAAAAGAGCCTGAAAAGTTTAAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268
Db	2026	GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA	2085
Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC	2328
Db	2086	TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTTC	2145
Qy	2329	TCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Db	2146	TCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2205
Qy	2389	GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTGAA	2448
Db	2206	GAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2265
Qy	2449	GTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2266	GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2325
Qy	2503	GTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
Db	2326	TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA	2385
Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
Db	2386	GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA	2445



Qy	2620	TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTT	2679
Db	2446	CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAGCTC	2505
Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA	2739
Db	2506	AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2565
Qy	2740	AGTGAAACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC	2799
Db	2566	ACTGAAACGTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATC	2625
Qy	2800	AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC	2856
Db	2626	AGTTCTAAAACTGATTCATTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC	2685
Qy	2857	GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCAATTGCCTTGCTTAGAATTG	2916
Db	2686	CACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCAATTGCCTTGCACAGAATTG	2745
Qy	2917	CCCTGTGACCTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA	2970
Db	2746	CCCCATGACCTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA	2805
Qy	2971	GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC	3030
Db	2806	GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT	2865
Qy	3031	TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA	3090
Db	2866	TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA	2925
Qy	3091	GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGAGCTGTA	3150
Db	2926	GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	2985
Qy	3151	TTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG	3210
Db	2986	TTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG	3045
Qy	3211	AAGACTGGAGTGGTGTTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTGAGC	3270
Db	3046	AAGACTGGAGTGGTGTTTGGTGCCAGCCTATTCCTGCTGCTTTTCATTGACAGTATTCAGC	3105
Qy	3271	ATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG	3330
Db	3106	ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG	3165
Qy	3331	ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCA	3390
Db	3166	ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCA	3225
Qy	3391	TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT	3450
Db	3226	TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT	3285
Qy	3451	CTTGGTCATGTGAACAGCACAAATAAAGAAGCTGAGGCGGCTTTTCTTAGTTGATGATTTA	3510





Qy	373	GAGGAGGACGAGGAGGAGGACGAGCAGGAGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG	432
Db	115	GAGGAGGAAGAGGAGGAGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG	174
Qy	433	CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCGCCGCCGCCGCCGCCGCTG	486
Db	175	CCCGCCGCCGGGCTGTCCGCAGGCCCCAGTGCCACCGCCCTGCCGCCGGCGCGCCCCCTG	234
Qy	487	CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCCC	546
Db	235	ATGGACTTCGGAAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC	294
Qy	547	CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC	597
Db	295	CCCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCTGTCGACCGTGCCC	354
Qy	598	GCGCCATCCCTGCCGCCCGCTGCCGCAGTCTGCCCTCCAAGCTCCCAGAGGACGACGAG	657
Db	355	GCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG	414
Qy	658	CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG-----	711
Db	415	CCTCCGGCCCCGGCCTCCCCCTCTCCCCGGCCAGCGTGAGCCCCAGGCAGAGCCCGTG	474
Qy	712	-----CCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC	750
Db	475	TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCGCGCCGCGCCCAAGCGC	534
Qy	751	AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTTGCTCTTCTGCTGCATCTGAGCCT	807
Db	535	AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTTCTGCTGCATCTGAGCCT	594
Qy	808	GTGATACCCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT	867
Db	595	GTGATACGCTCCTCTGCAGAAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT	651
Qy	868	TCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCTTCT	927
Db	652	TCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCTTCT	711
Qy	928	CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA	987
Db	712	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	771
Qy	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Db	772	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	831
Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Db	832	GAGAAGGCAAAAACCTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC	891
Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Db	892	TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	951

Qy	1168	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAAGAGGATTTAGTTTGTAGT	1224
Db	952	AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1011
Qy	1225	GCAGCCCTTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC	1269
Db	1012	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1071
Qy	1270	AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA	1329
Db	1072	GAAGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGAA	1131
Qy	1330	GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA	1389
Db	1132	GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA	1191
Qy	1390	GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG	1437
Db	1192	GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG	1248
Qy	1438	GAAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAGTCTTGGAAG	1497
Db	1249	GAAAGTAAAGTGGATAAAAAATGTTTGCAGATAGCCTTGAGCAAATAATCACGAAAAA	1308
Qy	1498	GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC	1557
Db	1309	GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT	1368
Qy	1558	AGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCT---CAGCAACCGAAAGCACCACA	1614
Db	1369	CGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA	1428
Qy	1615	GCAAACACTTTCCCTTTGTTAGAAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA	1674
Db	1429	ACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAA	1488
Qy	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT	1731
Db	1489	ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAAC	1548
Qy	1732	CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Db	1549	CCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA	1608
Qy	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG	1851
Db	1609	AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG	1668
Qy	1852	GAAGCATGTGAAAGTGAATGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Db	1669	GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA	1728
Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Db	1729	ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT	1788
Qy	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCTGATATTGTTATG	2031

Db	1789	TGCCCATCATTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG	1848
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA	2091
Db	1849	GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA	1908
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAAGCTTGAGCCTGAAAAC	2151
Db	1909	TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	1965
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	1966	CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA	2025
Qy	2209	GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268
Db	2026	GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA	2085
Qy	2269	TCCATTGCGTGTGATTAAATTAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC	2328
Db	2086	TCTATTGCATGTGATTAAATTAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTTC	2145
Qy	2329	TCTAATTATTGAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Db	2146	TCTGATTATTGAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2205
Qy	2389	GAGGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCCTGAA	2448
Db	2206	GAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2265
Qy	2449	GTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2266	GTTCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2325
Qy	2503	GTGTCTGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
Db	2326	TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA	2385
Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
Db	2386	GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA	2445
Qy	2620	TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTT	2679
Db	2446	CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTC	2505
Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA	2739
Db	2506	AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2565
Qy	2740	AGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCCACGTTTGTC	2799
Db	2566	ACTGAAACGTTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCTACATTGATC	2625
Qy	2800	AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC	2856

Db	2626	AGTTCTAAAAGTGAATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAAGTATCC	2685
Qy	2857	GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGAGATTTCATTGCCTTGCTTAGAATTG	2916
Db	2686	CACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCATTGCCTTGACACAGAATTG	2745
Qy	2917	CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA	2970
Db	2746	CCCCATGACCTTTCTTTGAAGAACATAACAACCAAAGTTGAAGAGAAAATCAGTTTCTCA	2805
Qy	2971	GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC	3030
Db	2806	GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT	2865
Qy	3031	TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA	3090
Db	2866	TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA	2925
Qy	3091	GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA	3150
Db	2926	GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	2985
Qy	3151	TTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG	3210
Db	2986	TTTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG	3045
Qy	3211	AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCTGCTGCTGTCTCTGACAGTGTTCAGC	3270
Db	3046	AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCTGCTGCTTTTCATTGACAGTATTTCAGC	3105
Qy	3271	ATTGTCAGTGTAACGGCCTACATTGCCTTGCCCTGCTCTCGGTGACTATCAGCTTTAGG	3330
Db	3106	ATTGTGAGCGTAACAGCCTACATTGCCTTGCCCTGCTCTCTGTGACCATCAGCTTTAGG	3165
Qy	3331	ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA	3390
Db	3166	ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA	3225
Qy	3391	TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT	3450
Db	3226	TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT	3285
Qy	3451	CTTGGTCATGTGAACAGCACAAATAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA	3510
Db	3286	CTTGGTCATGTGAAGTGCACGATAAAGGAAGTACAGGCGCCTCTTCTTAGTTGATGATTTA	3345
Qy	3511	GTTGATTCCCTGAAGTTTGCAGTGTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT	3570
Db	3346	GTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT	3405
Qy	3571	AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT	3630
Db	3406	AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT	3465
Qy	3631	GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT	3690
Db	3466	GAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT	3525

Qy 3691 GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740  
 || ||||| |||||||||||||||||||||||||||||||| ||  
 Db 3526 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3575

RESULT 13

AAD01174

ID AAD01174 standard; cDNA; 3833 BP.

XX

AC AAD01174;

XX

DT 02-NOV-2000 (first entry)

XX

DE Bovine neurite growth inhibitor Nogo cDNA.

XX

KW Bovine; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;  
 KW central nervous system; neoplastic disease; antiproliferative; glioma;  
 KW antisense gene therapy; neuroblastoma; menangioma; retinoblastoma;  
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
 KW structural plasticity; screening; ss.

XX

OS Bos sp.

XX

PN WO200031235-A2.

XX

PD 02-JUN-2000.

XX

PF 05-NOV-1999; 99WO-US026160.

XX

PR 06-NOV-1998; 98US-0107446P.

XX

PA (SCHW/) SCHWAB M E.

PA (CHEN/) CHEN M S.

XX

PI Schwab ME, Chen MS;

XX

DR WPI; 2000-400052/34.

XX

PT Nogo proteins and nucleic acids useful for treating neoplastic disorders  
 PT of the central nervous system and inducing regeneration of neurons.

XX

PS Claim 26; Fig 12; 122pp; English.

XX

CC The present sequence is a cDNA encoding bovine Nogo protein which is a  
 CC potent neural cell growth inhibitor and is free of all central nervous  
 CC system (CNS) myelin material with which it is natively associated. The  
 CC present sequence was obtained from bovine spinal cord white matter cDNA  
 CC library. Nogo proteins and fragments displaying neurite growth inhibitory  
 CC activity are used in the treatment of neoplastic disease of the CNS e.g.  
 CC glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma,  
 CC pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma,  
 CC menangioma, neuroblastoma or retinoblastoma and degenerative nerve  
 CC diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which  
 CC promote Nogo activity can be used to treat or prevent hyperproliferative





Qy	1495	AAGGATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAG	1554
Db	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA	660
Qy	1555	GACAGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACA	1614
Db	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACCCAACAACCTGAGAATGTTTCA	720
Qy	1615	GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA	1674
Db	721	ACAAACATTTTCCCTTGTGGAAGATCATACTTCGGAATAAAGACAGATGAAAAAAG	780
Qy	1675	ATAGAAGAAAGGAAGGCCAAATTATAACAGAGAAGA--CTAGCCCCAAAACGTCAAAT	1731
Db	781	ATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCAAAC	839
Qy	1732	CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Db	840	CCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTGTCA	899
Qy	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG	1851
Db	900	AAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTTCAG	959
Qy	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Db	960	GAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACAAAA	1019
Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Db	1020	ATGGACCTGGTTCAAACTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAGCTT	1079
Qy	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	2031
Db	1080	TGCCCATCTTTGAAGAATCTGAAGCTACTCCGTCACCGTTTTGCCTGACATTGTCATG	1139
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCAGTGTA	2091
Db	1140	GAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGTTCA	1199
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Db	1200	TCACCATTAGAAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAAAAT	1259
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	1260	CCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAATGAA	1319
Qy	2209	GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTTCAGGAAACAGAAGCTCCTTATATA	2268
Db	1320	GAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTTCAGGAAACAGAAGCTCCTTATATA	1379
Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC	2328
Db	1380	TCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGATTTTC	1439

Qy	2329	TCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Db	1440		
Qy	2389	TCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTAGTT	1499
Qy	2389	GAGGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCCTGAA	2448
Db	1500		
Qy	1500	GAAGATTCCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCCGAA	1559
Qy	2449	GTCCCAACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTC-	2507
Db	1560		
Qy	1560	GTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATTTCA	1619
Qy	2508	-----TGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCCTCAC---CTCAGGAG	2559
Db	1620		
Qy	1620	TCTGAGTCAATGACAGGACATGACAATAAGGGAAACTCAGTGCTTCACCATCACCTGAG	1679
Qy	2560	CTAGGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---T	2616
Db	1680		
Qy	1680	GGAGGAAAACCGTATTTGGAGTCTTTTCAGCCAGTTTAGGCATCACAAAAGATACCTTA	1739
Qy	2617	GCATCTAATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAG	2676
Db	1740		
Qy	1740	GCACCTGATGAAGTTTCAGCATTGACCAAAAAGGAGAAAAATCCCTTTGCAGATGGAGGAG	1799
Qy	2677	TTTAATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAA	2736
Db	1800		
Qy	1800	CTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTAAGA	1859
Qy	2737	GAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTT	2796
Db	1860		
Qy	1860	GAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACCTTT	1919
Qy	2797	GTCAGTGCTAA--AGATGATTCTCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTA	2853
Db	1920		
Qy	1920	GTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAAGTA	1979
Qy	2854	TCCGACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAA	2913
Db	1980		
Qy	1980	GCCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCAATTGGCTTGTGCAGGA	2039
Qy	2914	TTGCCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAGTACATGTTTCAGAT	2973
Db	2040		
Qy	2040	TTGCCCCATGACCTTTCTTTCAAGAGTATACAACCTAAAGAGGAAGTTCATGTCCAGAT	2099
Qy	2974	GAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTCTCT	3033
Db	2100		
Qy	2100	GAGTTCTCCAAGATAGGGGTGATGTTTCAAAGGTGCCCCGACTGCCTCCAGATGTTTCT	2159
Qy	3034	GCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAAGAA	3093
Db	2160		
Qy	2160	GCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTTGTGAAAGAA	2219
Qy	3094	GCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGAGCTGTATTG	3153
Db	2220		
Qy	2220	GCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCTGCTATATTT	2279
Qy	3154	TCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAG	3213

Db	2280	TCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAG	2339
Qy	3214	ACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATT	3273
Db	2340	ACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCCTGCTGCTCTCGCTGACAGTATTCAGCATT	2399
Qy	3274	GTCAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATA	3333
Db	2400	GTGAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATA	2459
Qy	3334	TATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATAT	3393
Db	2460	TATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTTCAGGGCATAT	2519
Qy	3394	TTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTT	3453
Db	2520	TTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTT	2579
Qy	3454	GGTCATGTGAACAGCACATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTT	3513
Db	2580	GGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTT	2639
Qy	3514	GATTCCCTGAAGTTTGCAGTGTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAAT	3573
Db	2640	GATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAAT	2699
Qy	3574	GGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAA	3633
Db	2700	GGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAA	2759
Qy	3634	CGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCC	3693
Db	2760	CGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCT	2819
Qy	3694	ATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA	3740
Db	2820	ATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGA	2866

RESULT 14

AAV30920

ID AAV30920 standard; cDNA; 2386 BP.

XX

AC AAV30920;

XX

DT 14-SEP-1998 (first entry)

XX

DE Human secreted protein BG160\_1 cDNA.

XX

KW BG160\_1; secreted protein; protein factor; human; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 102..2030

FT /\*tag= a

FT sig\_peptide 1863. .1899  
 FT /\*tag= b  
 FT /note= "putative leader/signal peptide"  
 FT mat\_peptide 1900. .2027  
 FT /\*tag= c  
 XX  
 PN WO9817687-A2.  
 XX  
 PD 30-APR-1998.  
 XX  
 PF 24-OCT-1997; 97WO-US019590.  
 XX  
 PR 25-OCT-1996; 96US-00740274.  
 PR 24-OCT-1997; 97US-00740274.  
 XX  
 PA (GEMY ) GENETICS INST INC.  
 XX  
 PI Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;  
 PI Spaulding V, Agostino MJ;  
 XX  
 DR WPI; 1998-261426/23.  
 DR P-PSDB; AAW58383.  
 XX  
 PT Nucleic acid encoding secreted protein from human cells - useful, e.g. as  
 PT immuno-modulators, anti-tumour agents, promoters of tissue growth,  
 PT haemostatic and thrombolytic agents etc.  
 XX  
 PS Claim 20; Page 74-75; 114pp; English.  
 XX  
 CC This cDNA clone, designated BG160\_1, codes for a novel human secreted  
 CC protein (see AAW58383). It was isolated from a human adult brain cDNA  
 CC library using methods selective for cDNAs that encode secreted proteins.  
 CC The clone is deposited in composite clone ATCC 98232; an oligonucleotide  
 CC (see AAT99725) is designed to isolate the clone from the composite. The  
 CC predicted AT415\_4 amino acid sequence shows homology to neuroendocrine-  
 CC specific proteins. Novel cDNA clones (see AAV30916-32) coding for human  
 CC secreted proteins (see AAW58580-90) are claimed. These can be used for  
 CC recombinant production of the secreted proteins for analysis,  
 CC characterisation, diagnostic or therapeutic use. They can also be used as  
 CC tissue or mol.wt. markers, for chromosome identification, to identify  
 CC genetic disorders, to isolate new related DNA, as sources of primers for  
 CC PCR, to generate antibodies, and in interaction trap assays. The secreted  
 CC proteins may also have many biological activities, e.g. cytokine,  
 CC immunomodulator, haematopoiesis regulating activity, tissue growth  
 CC activity, activin or inhibin activity, chemotactic or chemokinetic  
 CC activity, haemostatic and thrombolytic activity, receptor/ligand  
 CC activity, antiinflammatory, cadherin and tumour invasion suppressor  
 CC activity, and tumour inhibition activity. The proteins can be expressed  
 CC in vivo from DNA, introduced in gene therapy vectors  
 XX  
 SQ Sequence 2386 BP; 756 A; 450 C; 494 G; 686 T; 0 U; 0 Other;

Query Match 37.7%; Score 1411.2; DB 2; Length 2386;  
 Best Local Similarity 83.3%; Pred. No. 5e-288;  
 Matches 1702; Conservative 0; Mismatches 303; Indels 39; Gaps 7;

Qy 1718 CCAAAACGTCAAATCCTTCTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAA 1777

Db	1	CCAAAACATCAAACCCCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAA	60
Qy	1778	CAGATACCTTATCAAAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGC	1837
Db	61	CAGATAATTTAACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTC	120
Qy	1838	CAGATTTAGTTCAGGAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTG	1897
Db	121	CAGATTTAGTACAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTG	180
Qy	1898	CTTATGAAACAAAAGTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACC	1957
Db	181	CTTATGAAACAAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATC	240
Qy	1958	CCACAGCACAGCTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGC	2017
Db	241	CTGCAGCACAGCTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGC	300
Qy	2018	CTGATATTGTTATGGAAGCACCATTAAATCTCTCCTTCCAAGCGCTGGTGCTTCTGTAG	2077
Db	301	CTGACATTGTTATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGA	360
Qy	2078	TGCAGCCCAGTGTATCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGC	2137
Db	361	TACAGCCCAGCTCATCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAAC	417
Qy	2138	TTGAGCCTGAAAACCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTT	2194
Db	418	ATGAGCCTGAAAACCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTAT	477
Qy	2195	TGGGAACAAAGGAAGGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAG	2254
Db	478	CAGGAATAAAGGAAGAAATTAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAG	537
Qy	2255	AAGCTCCTTATATATCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGC	2314
Db	538	AAGCTCCTTATATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAAC	597
Qy	2315	CAAGTCCAGATTTCTCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAAC	2374
Db	598	CAGCTCCGATTTCTCTGATTATTCAGAAATGGCAAAGTTGAACAGCCAGTGCCTGATC	657
Qy	2375	ACGCTGAGCTAGTGGAGGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATG	2434
Db	658	ATTCTGAGCTAGTTGAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATG	717
Qy	2435	ATTGATTCCTGAAGTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTC	2494
Db	718	ATTCAATACCTGACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTC	777
Qy	2495	TCACTGA-----AGTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCT	2548
Db	778	TCACTGAGACTTCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCTT	837
Qy	2549	CACCTCAGGAGCTAGGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAA	2608

[illegible]

Qy 3437 ACAGTAATTCTGCTCTTGGTCATGTGAACAGCACATAAAAGAACTGAGGCGGCTTTTCT 3496  
 |||||  
 Db 1723 ACAGTAATTCTGCTCTTGGTCATGTGAACAGCACATAAAGGAACCTCAGGCGCCTCTTCT 1782  
 Qy 3497 TAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATG 3556  
 |||||  
 Db 1783 TAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATG 1842  
 Qy 3557 TTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTA 3616  
 |||||  
 Db 1843 TTGGTGCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTG 1902  
 Qy 3617 TTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACA 3676  
 |||||  
 Db 1903 TTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATA 1962  
 Qy 3677 AGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG 3736  
 |||||  
 Db 1963 AGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG 2022  
 Qy 3737 CAGA 3740  
 ||  
 Db 2023 CTGA 2026

# RESULT 15

AAF98399

ID AAF98399 standard; cDNA; 2386 BP.

XX

AC AAF98399;

XX

DT 07-JUN-2001 (first entry)

XX

DE Human cDNA clone BG160\_1 sequence SEQ ID 41.

XX

KW Human; secreted protein; nutrient; cytokine modulator; proliferation;  
 KW differentiation; immune system modulator; tissue growth; chemotactic;  
 KW haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;  
 KW haematopoiesis.

XX

OS Homo sapiens.

XX

PN WO200119988-A1.

XX

PD 22-MAR-2001.

XX

PF 14-SEP-2000; 2000WO-US025135.

XX

PR 17-SEP-1999; 99US-00398829.

XX

PA (GEMY ) GENETICS INST INC.

XX

PI Jacobs K, Mccoy JM, Lavallie ER, Collins-Racie LA, Evans C;

PI Merberg D, Treacy M, Bowman MR, Spaulding V, Agostino MJ;

XX

DR WPI; 2001-244801/25.



DR P-PSDB; AAB90682.  
 XX  
 PT Isolated nucleic acids encoding polypeptides, useful for modulating e.g.  
 PT cytokine and cell proliferation/differentiation activity, the immune  
 PT system and hematopoiesis regulating activity.  
 XX  
 PS Claim 1; Page 408-409; 557pp; English.  
 XX  
 CC Human cDNA clones represented in AAF98374 - AAF98489 encode secreted  
 CC proteins AAB90667 - AAB90750. The cDNA clones are isolated from various  
 CC tissue types, and may be used in the prevention, treatment and diagnosis  
 CC of diseases associated with inappropriate protein expression. The  
 CC polypeptides and nucleic acids may be used as nutrients or to modulate  
 CC cytokine and cell proliferation/differentiation activity and may also be  
 CC involved in modulation of the immune system. The cDNA sequences,  
 CC proteins, their agonists and/or antagonists exhibit haematopoiesis  
 CC regulating activity; tissue growth activity; activin/inhibin activity;  
 CC chemotactic/chemokinetic activity; haemostatic and thrombolytic activity;  
 CC receptor/ligand activity; anti-inflammatory activity; haematopoiesis  
 CC activity; cadherin/tumour suppressor activity; and/or tumour inhibition  
 CC activity. Included in the invention are probes represented in AAF98490 -  
 CC AAF98572 which are specific for the cDNA clones encoding the secreted  
 CC proteins  
 XX  
 SQ Sequence 2386 BP; 756 A; 448 C; 496 G; 686 T; 0 U; 0 Other;

Query Match 37.6%; Score 1408; DB 5; Length 2386;  
 Best Local Similarity 83.2%; Pred. No. 2.4e-287;  
 Matches 1700; Conservative 0; Mismatches 305; Indels 39; Gaps 7;

Qy	1718	CCAAAACGTCAAATCCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAA	1777
Db	1	CCAAAACATCAAACCCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAA	60
Qy	1778	CAGATACCTTATCAAAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGC	1837
Db	61	CAGATAATTTAACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTC	120
Qy	1838	CAGATTTAGTTCAGGAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTG	1897
Db	121	CAGATTTAGTACAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTG	180
Qy	1898	CTTATGAAACAAAAGTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACC	1957
Db	181	CTTATGAAACAAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATC	240
Qy	1958	CCACAGCACAGCTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGC	2017
Db	241	CTGCAGCACAGCTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGC	300
Qy	2018	CTGATATTGTTATGGAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAG	2077
Db	301	CTGACATTGTTATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGA	360
Qy	2078	TGCAGCCCAGTGTATCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGC	2137
Db	361	TACAGCCCAGCTCATCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAAC	417

Qy 2138 TTGAGCCTGAAAACCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTT 2194  
 |||||  
 Db 418 ATGAGCCTGAAAACCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTAT 477

Qy 2195 TGGGAACAAAGGAAGGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAG 2254  
 |||||  
 Db 478 CAGGAATAAAGGAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAG 537

Qy 2255 AAGCTCCTTATATATCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGC 2314  
 |||||  
 Db 538 AAGCTCCTTATATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAAC 597

Qy 2315 CAAGTCCAGATTTCTCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAAC 2374  
 |||||  
 Db 598 CAGCTCCGGATTTCTCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATC 657

Qy 2375 ACGCTGAGCTAGTGGAGGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATG 2434  
 |||||  
 Db 658 ATTCTGAGCTAGTTGAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATG 717

Qy 2435 ATTCGATTCCCTGAAGTCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTC 2494  
 |||||  
 Db 718 ATTCAATACCTGACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTC 777

Qy 2495 TCACTGA-----AGTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCT 2548  
 |||||  
 Db 778 TCACTGAGACTTCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTT 837

Qy 2549 CACCTCAGGAGCTAGGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAA 2608  
 |||||  
 Db 838 TGCCACCTGAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAA 897

Qy 2609 AAGATGC---TGCATCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGC 2665  
 |||||  
 Db 898 AAGATACCCTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGC 957

Qy 2666 AAATGGAAGAGTTTAATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAG 2725  
 |||||  
 Db 958 AGATGGAGGAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAG 1017

Qy 2726 ACAAATAAAAAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAAT 2785  
 |||||  
 Db 1018 CACAGATAAGAGAAACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGT 1077

Qy 2786 TTCCACGTTTGTGAGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTG 2842  
 |||||  
 Db 1078 TCCCTACATTGATCAGTTCTAAACTGATTCAATTTCTAAATTAGCCAGGGAATATACTG 1137

Qy 2843 ATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTTCATTGC 2902  
 |||||  
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Qy 2903 CTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG--- 2959  
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Db	1498	GGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTCAT	1557
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Qy	3317	CTATCAGCTTTAGGATATATAAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCC	3376
Db	1618	CCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCC	1677
Qy	3377	ACCCATTTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAAT	3436
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Qy	3677	AGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG	3736
Db	1963	AGAATGTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG	2022
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Db	2023	CTGA 2026	

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Job time : 1328.89 secs

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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 01:30:35 ; Search time 232.145 Seconds  
(without alignments)  
8942.975 Million cell updates/sec

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Perfect score: 3741  
Sequence: 1 attgctcgtctctgggcggcgg.....gattgaagcgcaaagcagat 3741

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2323.8	62.1	4822	4	US-09-484-970B-106	Sequence 106, App
2	497.4	13.3	799	2	US-08-700-607-2	Sequence 2, Appli
3	484.8	13.0	2610	4	US-09-023-655-382	Sequence 382, App
4	228.8	6.1	1766	4	US-09-149-476-254	Sequence 254, App
5	228.8	6.1	2664	4	US-09-149-476-255	Sequence 255, App
6	203.6	5.4	1095	2	US-08-700-607-4	Sequence 4, Appli
7	198	5.3	454	4	US-09-621-976-740	Sequence 740, App
8	196.6	5.3	463	4	US-09-621-976-741	Sequence 741, App
9	180.4	4.8	794	4	US-09-149-476-102	Sequence 102, App
10	164.6	4.4	261	2	US-08-700-607-9	Sequence 9, Appli
c 11	75.4	2.0	7218	1	US-08-232-463-14	Sequence 14, Appl

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c	14	73.2	2.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli
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	16	71.8	1.9	1614	4	US-09-616-289-45	Sequence 45, Appl
	17	71.8	1.9	12425	4	US-09-616-289-50	Sequence 50, Appl
c	18	68.6	1.8	319	3	US-09-165-264-8	Sequence 8, Appli
	19	68	1.8	4403765	3	US-09-103-840A-2	Sequence 2, Appli
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	36	63.6	1.7	38506	3	US-09-320-878-19	Sequence 19, Appl
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c	45	60.6	1.6	12001	1	US-08-458-568A-11	Sequence 11, Appl

#### ALIGNMENTS

##### RESULT 1

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US-09-484-970B-106
; Sequence 106, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmuth, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 106
; LENGTH: 4822
; TYPE: DNA
; ORGANISM: Homo sapiens

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; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. 6426186 444857.15CB1  
; NAME/KEY: unsure  
; LOCATION: 33, 51, 79, 211, 369, 483-484, 731, 748, 4803, 4805-4806, 4808-4809,  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-484-970B-106

Query Match 62.1%; Score 2323.8; DB 4; Length 4822;  
Best Local Similarity 80.9%; Pred. No. 0;  
Matches 3060; Conservative 0; Mismatches 587; Indels 137; Gaps 25;

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Qy     362 ACGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGC 421
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Db	1910	AGATTTAGTACAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGC	1969
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Db	1970	TTATGAAACAAAATGGACTTGGTTCAAACATCAGAAAGTTATGCAAGAGTCACTCTATCC	2029
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Db	2567	CACTGAGACTTCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCTTT	2626
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 Db 3467 ACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAAT 3526  
 Qy 3437 ACAGTAATTCTGCTCTTGGTCATGTGAACAGCACATAAAAGAACTGAGGCGGCTTTTCT 3496  
 |||  
 Db 3527 ACAGTAATTCTGCTCTTGGTCATGTGAACAGCACATAAAAGAACTGAGGCGCCTCTTCT 3586  
 Qy 3497 TAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAAGTTGATGTGGGTGTTTACTTATG 3556  
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 Db 3587 TAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAAGTTGATGTGGGTATTTACCTATG 3646  
 Qy 3557 TTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTA 3616  
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 Db 3647 TTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTG 3706  
 Qy 3617 TTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACA 3676  
 |||  
 Db 3707 TTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATA 3766  
 Qy 3677 AGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG 3736  
 |||  
 Db 3767 AGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG 3826  
 Qy 3737 CAGA 3740  
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 Db 3827 CTGA 3830

RESULT 2

US-08-700-607-2

; Sequence 2, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

```

; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 799 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
US-08-700-607-2

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Query Match          13.3%; Score 497.4; DB 2; Length 799;
Best Local Similarity 92.7%; Pred. No. 1.4e-106;
Matches 522; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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Qy      3178 GTTGTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 3237
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Db      108 GTTGTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 167

Qy      3238 TTATTCCTGCTGCTGTCTCTGACAGTGTTGAGCATTGTGAGTGTAACGGCCTACATTGCC 3297
          |||
Db      168 CTATTCCTGCTGCTTTTCATTGACAGTATTGAGCATTGTGAGCGTAACAGCCTACATTGCC 227

Qy      3298 TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATC 3357
          |||
Db      228 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 287

Qy      3358 CAGAAATCAGATGAAGGCCACCCATTGAGGGCATATTTAGAATCTGAAGTTGCTATATCA 3417
          |||
Db      288 CAGAAATCAGATGAAGGCCACCCATTGAGGGCATATCTGGAATCTGAAGTTGCTATATCT 347

Qy      3418 GAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAA 3477
          |||
Db      348 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAAGTGCACGATAAAG 407

Qy      3478 GAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTG 3537
          |||
Db      408 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 467

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Qy 3538 ATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCT 3597  
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 Db 468 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT 527  
 Qy 3598 CTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCAT 3657  
 || || |  
 Db 528 CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 587  
 Qy 3658 TATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATC 3717  
 ||||| |||| |  
 Db 588 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 647  
 Qy 3718 CCTGGATTGAAGCGCAAAGCAGA 3740  
 ||||| ||  
 Db 648 CCTGGATTGAAGCGCAAAGCTGA 670

RESULT 3

US-09-023-655-382

; Sequence 382, Application US/09023655

; Patent No. 6607879

; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.

; APPLICANT: Susan G. Stuart

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

; TITLE OF INVENTION: EXPRESSION

; NUMBER OF SEQUENCES: 1508

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/023,655

; FILING DATE: HEREWITH

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071

; REFERENCE/DOCKET NUMBER: PA-0001 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 855-0555

; TELEFAX: (650) 845-4166

; INFORMATION FOR SEQ ID NO: 382:

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; SEQUENCE CHARACTERISTICS:
;   LENGTH: 2610 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: LUNGNOT14
;   CLONE: 1508778
US-09-023-655-382

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Query Match          13.0%; Score 484.8; DB 4; Length 2610;
Best Local Similarity 92.4%; Pred. No. 2.4e-103;
Matches 521; Conservative 0; Mismatches 42; Indels 1; Gaps 1;

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Qy      3178 GTTGTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 3237
          |||
Db      1311 GTTGTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 1370
          |||

Qy      3238 TTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAAACGGCCTAC-ATTGC 3296
          |||
Db      1371 CTATTCCTGCTGCTTTCATTGACAGTATTGAGCATTGTGAGCGTAACAGCCTACAATTGC 1430
          |||

Qy      3297 CTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTAT 3356
          |||
Db      1431 CTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGGTGTGATCCAAGCTAT 1490
          |||

Qy      3357 CCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATC 3416
          |||
Db      1491 CCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATC 1550
          |||

Qy      3417 AGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAA 3476
          |||
Db      1551 TGAGGAGTTGGTTCAGAAAGTACAGTAATTCTGCTCTTGGTCATGTGAAGTGCACGATAAA 1610
          |||

Qy      3477 AGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGAGTGT 3536
          |||
Db      1611 GGAATCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGAGTGT 1670
          |||

Qy      3537 GATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGC 3596
          |||
Db      1671 GATGTGGGTATTTACCTATGTTGGTGCCTTGTTAATGGTCTGACACTACTGATTTTGGC 1730
          |||

Qy      3597 TCTGATCTCACTCTTCAGTATTCCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCA 3656
          |||
Db      1731 TCTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCA 1790
          |||

Qy      3657 TTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAAT 3716
          |||
Db      1791 TTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAAT 1850
          |||

Qy      3717 CCCTGGATTGAAGCGCAAAGCAGA 3740
          |||
Db      1851 CCCTGGGTTGAAGCGCAAAGCTGA 1874
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RESULT 4  
 US-09-149-476-254

; Sequence 254, Application US/09149476  
; Patent No. 6420526  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: PZ002P1  
; CURRENT APPLICATION NUMBER: US/09/149,476  
; CURRENT FILING DATE: 1998-09-08  
; EARLIER APPLICATION NUMBER: PCT/US98/04493  
; EARLIER FILING DATE: 1998-03-06  
; EARLIER APPLICATION NUMBER: 60/040,162  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,333  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/038,621  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,626  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,334  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,336  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,163  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/047,600  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,615  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,597  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,502  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,633  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,583  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,617  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,618  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,503  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,592  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,581  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,584  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,500  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,587  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,492  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,598  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,613

; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,582  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,596  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,612  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,632  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,601  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,580  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,568  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,314  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,569  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,311  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,671  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,674  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,669  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,312  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,313  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,672  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,315  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/048,974  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/056,886  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,877  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,889  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,893  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,630  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,878  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,662  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,872  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,882  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,637  
; EARLIER FILING DATE: 1997-08-22



; EARLIER APPLICATION NUMBER: 60/056,903  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,888  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,879  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,880  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,894  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,911  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,636  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,874  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,910  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,864  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,631  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,845  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,892  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/057,761  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/047,595  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,599  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,588  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,585  
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; EARLIER APPLICATION NUMBER: 60/047,586  
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; EARLIER APPLICATION NUMBER: 60/047,590  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,594  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,589  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,593  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,614  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,578  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,576  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/047,501  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,670  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/056,632

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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

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Query Match          6.1%;  Score 228.8;  DB 4;  Length 1766;
Best Local Similarity 63.4%;  Pred. No. 1.3e-43;
Matches 350;  Conservative 0;  Mismatches 202;  Indels 0;  Gaps 0;

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Qy      3174 TTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGC 3233
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Db      286  TGCGGTGCACGATCTGATTTTCTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCAC 345

Qy      3234 CAGCTTATTCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTTCAGTGTAACGGCCTACAT 3293
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      346  CACGCTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTCATCAGTGTTGTTTCTTACCT 405

Qy      3294 TGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGC 3353
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      406  CATCCTGGCTCTTCTCTCTGTCAACCATCAGCTTCAGGATCTACAAGTCCGTATCCAAGC 465

Qy      3354 TATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATTTAGAATCTGAAGTTGCTAT 3413
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      466  TGTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCT 525

Qy      3414 ATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAAT 3473
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      526  GTCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGCACATCAACAGGGCCCT 585

Qy      3474 AAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGT 3533
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      586  GAAACTCATTATTTCGTCTCTTTCTGGTAGAAGATCTGGTTGACTCCTTGAAGCTGGCTGT 645

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QY 3534 GTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTT 3593  
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 Db 646 CTTTCATGTGGCTGATGACCTATGTTGGTGTCTGTTTTTAACGGAATCACCCCTTCTAATTCT 705

QY 3594 AGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGA 3653  
 ||| | | ||||| | || | ||||| | | || ||||| ||  
 Db 706 TGCTGAAGTGTCTCATTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGATTGA 765

QY 3654 TCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAA 3713  
 ||| ||| | || | || | || || || ||||| |||||  
 Db 766 TCACTATGTTGGCATCGCCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAA 825

QY 3714 AATCCCTGGATT 3725  
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 Db 826 ACTCCCTGGAAT 837

RESULT 5

US-09-149-476-255

; Sequence 255, Application US/09149476  
 ; Patent No. 6420526  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: 186 Human Secreted proteins  
 ; FILE REFERENCE: PZ002P1  
 ; CURRENT APPLICATION NUMBER: US/09/149,476  
 ; CURRENT FILING DATE: 1998-09-08  
 ; EARLIER APPLICATION NUMBER: PCT/US98/04493  
 ; EARLIER FILING DATE: 1998-03-06  
 ; EARLIER APPLICATION NUMBER: 60/040,162  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/040,333  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/038,621  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/040,626  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/040,334  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/040,336  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/040,163  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/047,600  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,615  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,597  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,502  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,633  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,583  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,617

; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,618  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,503  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,592  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,581  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,584  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,500  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,587  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,492  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,598  
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; EARLIER APPLICATION NUMBER: 60/047,613  
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; EARLIER APPLICATION NUMBER: 60/047,596  
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; EARLIER APPLICATION NUMBER: 60/047,601  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,580  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,568  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,314  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,569  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,311  
; EARLIER FILING DATE: 1997-04-11  
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; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,669  
; EARLIER FILING DATE: 1997-04-11  
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; EARLIER APPLICATION NUMBER: 60/043,672  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,315  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/048,974  
; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/056,886  
; EARLIER FILING DATE: 1997-08-22  
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; EARLIER APPLICATION NUMBER: 60/047,586

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; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
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; EARLIER APPLICATION NUMBER: 60/043,576
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

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Query Match          6.1%;   Score 228.8;   DB 4;   Length 2664;
Best Local Similarity 63.4%;   Pred. No. 1.6e-43;
Matches 350;   Conservative 0;   Mismatches 202;   Indels 0;   Gaps 0;

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Qy      3174 TTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGTC 3233
          | | | |   | | | | | | | | | | | | | | | | | | | | | | | |
Db      261  TCGGGTGCACGATCTGATTTTCTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCAC 320

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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1095 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: THPINOB01
; CLONE: 31870
US-08-700-607-4

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Query Match          5.4%; Score 203.6; DB 2; Length 1095;
Best Local Similarity 61.6%; Pred. No. 7.6e-38;
Matches 337; Conservative 1; Mismatches 208; Indels 1; Gaps 1;

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Qy      3174 TTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGTC 3233
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      328  TGCGGTGCACGATCTGATTTTMTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCAC 387

Qy      3234 CAGCTTATTCTGCTGCTGTCTCTGACAGTGTTGAGCATTGTCAGTGTAACGGCCTACAT 3293
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      388  CACGCTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTCATCAGTGTGGTTTCTTACCT 447

Qy      3294 TGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGC 3353
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      448  CATCCTGGCTCTTCTCTCTGTCAACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGC 507

Qy      3354 TATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTAT 3413
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      508  TGTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCT 567

Qy      3414 ATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAAAT 3473
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      568  GTCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGCACATCAACAGGGGCCCT 627

Qy      3474 AAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGT 3533
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Db      628  GAAACTCATTATTTCGTCTCTTTCTGGTAGAAGATCTGGTTGACTCCTTGAAGCTGGCTGT 687

Qy      3534 GTTGATGTGGGTGTTTACTTATGTTGGTGCCCTGTTCAATGGTCTGACACTACTGATTTT 3593
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      688  CTTCATGTGGCTGATGACCTATGTTGGTGCTGTTTTTAACGGAATCACCCCTTCTAATTCT 747

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Qy 3594 AGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGA 3653  
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 Db 748 TGCTGAACTGCTCATTTTNAAGTGTCCCGATTGTNTATNAGAAGTACAAGGTTT-CAAGCA 806

Qy 3654 TCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAA 3713  
 | | | | | | | | | | | | | | | | | | | |  
 Db 807 AAACCTCCCTGGAATCGCCAAAAAAAAGGCAGAATAAGTACATGGAAACCAGAAATGCAAC 866

Qy 3714 AATCCCT 3720  
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 Db 867 AGTTACT 873

RESULT 7

US-09-621-976-740  
 ; Sequence 740, Application US/09621976  
 ; Patent No. 6639063  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dumas Milne Edwards, J.B.  
 ; APPLICANT: Jobert, S.  
 ; APPLICANT: Giordano, J.Y.  
 ; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
 ; FILE REFERENCE: GENSET.054PR2  
 ; CURRENT APPLICATION NUMBER: US/09/621,976  
 ; CURRENT FILING DATE: 2000-07-21  
 ; NUMBER OF SEQ ID NOS: 19335  
 ; SOFTWARE: Patent.pm  
 ; SEQ ID NO 740  
 ; LENGTH: 454  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 229..453  
 US-09-621-976-740

Query Match 5.3%; Score 198; DB 4; Length 454;  
 Best Local Similarity 71.8%; Pred. No. 9.5e-37;  
 Matches 359; Conservative 7; Mismatches 72; Indels 62; Gaps 6;

Qy 19 GGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCGATCGCGAAGGCAGCAGAA 78  
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 Db 10 GGCGGCGGCGGCAAGTGGGGACAGGGCGGGTGGCGCATCACCGGCGCGSAGGCAGGAGGA 69

Qy 79 GCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTTCGGCTCGGCTCGGCACGA 138  
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 Db 70 GCAGTCTCATTGTTCCGGGAGCCGTCACCACAGTAGGTCCCTCGG----- 114

Qy 139 CTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACAACCGCCCGCGACTCTGAG 198  
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 Db 115 CTCAGTCGGCCCAGCCCCCTCTCAGTCTCCCCAACCCCCACAACCGCCCGCGGCTCTGAG 174

Qy 199 GAGAAGCGGC-CCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCCATGGA 257  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 175 ACGCGGCCCCGGCGGCGGCGGCGAGCAGCTGCAGCATCATC-TCCACCCTCCAGCCATGGA 233

Qy 258 AGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCGGCCTCCGCC 317  
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 Db 234 AGACCTGGACCAGTCTCCTCTGGT---CTCGTCCTCGGACAGCCACCCCGGCMGCAGCC 290  
 Qy 318 CGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAGGAGGA 377  
 ||| ||||| |||||: ||| ||||| ||||| |||||  
 Db 291 CGCGTTCAAGTACCAGTTCRTGAGGGAGCCCGAGGACGAGGAG----- 333  
 Qy 378 GGACGAGGAGGAGGACGACGAGGACCTAGAGGAACCTGGAGGTGCTGGAGAGGAAGCCCGC 437  
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 Db 334 -----GAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAGCCCGC 374  
 Qy 438 AGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCGCCGCCGCCGCCGCTGCTGGA 491  
 :||:|||||: ||| || | ||| | || ||: ||: | |||| | ||| |||  
 Db 375 MCGMGGGCTGTMCGCCGCCCCAGTGCMCACMCMCCTGCMGCMGGCGCGCCCTGATGGA 434  
 Qy 492 CTTACAGCAGCGACTCGGTGC 511  
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 Db 435 CTTGGAATGACTTCGTGC 454

RESULT 8

US-09-621-976-741  
 ; Sequence 741, Application US/09621976  
 ; Patent No. 6639063  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dumas Milne Edwards, J.B.  
 ; APPLICANT: Jobert, S.  
 ; APPLICANT: Giordano, J.Y.  
 ; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
 ; FILE REFERENCE: GENSET.054PR2  
 ; CURRENT APPLICATION NUMBER: US/09/621,976  
 ; CURRENT FILING DATE: 2000-07-21  
 ; NUMBER OF SEQ ID NOS: 19335  
 ; SOFTWARE: Patent.pm  
 ; SEQ ID NO 741  
 ; LENGTH: 463  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 237..461  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: 20  
 ; OTHER INFORMATION: n=a, g, c or t  
 US-09-621-976-741

Query Match 5.3%; Score 196.6; DB 4; Length 463;  
 Best Local Similarity 70.2%; Pred. No. 2e-36;  
 Matches 358; Conservative 12; Mismatches 78; Indels 62; Gaps 6;

Qy 10 CTGGGCGGCGGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCGATCGCGAAG 69  
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 Qy 70 GCAGCAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGTTCTTCGGCTCGGC 129  
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Db          69 GCAGGAGGAGCAGTCTCATTGTTCCGGGAGCCGTCACCACAGTAGGTCCCTCGG----- 122
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Db          123 -----CTCAGTCGGCCCAGCCCCTCTCAGTCCTCCCAACCCCCACAACCGCCCGC 173
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Db          174 GGCTCTGAGACGCGGCCCGGCGGCGGCGGCAGCAGCTGCAGCATCATC-TCCACCCTCC 232
QY          249 AGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCG 308
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Db          233 AGCCATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCCTCGGACAGCCACCCCG 289
QY          309 GCCTCCGCCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGA 368
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Db          290 GCMGCAGCCCGCGTTCAAGTACCAGTTCRTGAGGGAGCCCGAGGACGAGGAG----- 341
QY          369 GGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAG 428
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Db          342 -----GAAGACCTGGAGGAGCTGGAGGTGCTGGAGAG 373
QY          429 GAAGCCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCGCCGCCCGCCGCC 482
              ||||| |||||: ||: |||||: ||| || | |||| | || ||: ||: | |||||
Db          374 GAAGCCCGCMGCMGGGCTGTMC GCGGCCCCAGTGCMCACMGCMCTGCMGCMGGCGCGCC 433
QY          483 GCTGCTGGACTTCAGCAGCGACTCGGTGCC 512
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# RESULT 9

US-09-149-476-102

; Sequence 102, Application US/09149476

; Patent No. 6420526

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 186 Human Secreted proteins

; FILE REFERENCE: PZ002P1

; CURRENT APPLICATION NUMBER: US/09/149,476

; CURRENT FILING DATE: 1998-09-08

; EARLIER APPLICATION NUMBER: PCT/US98/04493

; EARLIER FILING DATE: 1998-03-06

; EARLIER APPLICATION NUMBER: 60/040,162

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,333

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/038,621

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,626

; EARLIER FILING DATE: 1997-03-07

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; EARLIER APPLICATION NUMBER: 60/043,580  
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; EARLIER APPLICATION NUMBER: 60/043,568  
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; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,671  
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; EARLIER APPLICATION NUMBER: 60/043,674

; EARLIER FILING DATE: 1997-04-11  
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; EARLIER APPLICATION NUMBER: 60/043,312  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,313  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,672  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,315  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/048,974  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/056,886  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,877  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,889  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,893  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,630  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,878  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,662  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,872  
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; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,903  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,888  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,879  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,880  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,894  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,911  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,636  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,874  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,910  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,864  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,631  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,845  
; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,892  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/057,761  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/047,595  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,599  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,588  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,585  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,586  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,590  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,594  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,589  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,593  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,614  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,578  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,576  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/047,501  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,670  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/056,632  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,664  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,876  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,881  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,909  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,875  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,862  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,887  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,908  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/048,964  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/057,650  
; EARLIER FILING DATE: 1997-09-05  
; EARLIER APPLICATION NUMBER: 60/056,884  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/057,669

; EARLIER FILING DATE: 1997-09-05  
; EARLIER APPLICATION NUMBER: 60/049,610  
; EARLIER FILING DATE: 1997-06-13  
; EARLIER APPLICATION NUMBER: 60/061,060  
; EARLIER FILING DATE: 1997-10-02

Query Match 4.8%; Score 180.4; DB 4; Length 794;  
Best Local Similarity 61.0%; Pred. No. 1.7e-32;  
Matches 332; Conservative 6; Mismatches 202; Indels 4; Gaps 3;

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Qy      3174 TTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGC 3233
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Db      253 TGCGGTGCACGATCTGATTTTCTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTG--GA 310

Qy      3234 CAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTACGATTGTCAGTGTAACGGCC--TACA 3292
          || | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      311 CACGCTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTCATCARTGTGGGTTTCTTAMC 370

Qy      3293 TTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGG 3352
          | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      371 TCATCCTGGCTCTTCTCTCTGTCAACCATCARCTTCAGGATCTACAAGTCCGTCATCCAAG 430

Qy      3353 CTATCCAGAAATCAGATGAAGGCCACCCATT--CAGGGCATATTTAGAATCTGAAGTTGCT 3411
          || | |||||:||||| :||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      431 CTGTWCAGAARTCAGAARAAGGCCATCCAWTCCAAAGCCTACCTGGACGTAGACATTACT 490

Qy      3412 ATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACA 3471
          | || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      491 CTGTCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGCACATCAACAGGGGCC 550

Qy      3472 ATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCA 3531
          | |||| | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      551 CTGAAACTCATTATTCGTCTCTTCTGGTAGAAGATCTGGTTGACTCCTTGAAGCTGGCT 610

Qy      3532 GTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATT 3591
          || || ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      611 GTCTTCATGTGGCTGATGACCTATGTTGGTGTCTTTTTTAACGGAATCACCCCTTCTAATT 670

Qy      3592 TTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATA 3651
          | |||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      671 CTTGCTGAACTGCTCATTTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGATT 730

Qy      3652 GATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCA 3711
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      731 GATCACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCCAAGC 790

Qy      3712 AAAA 3715
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Db      791 AAAA 794
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RESULT 10

US-08-700-607-9

; Sequence 9, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga

```

; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 261 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: SPLNFET01
; CLONE: 28742
US-08-700-607-9

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Query Match          4.4%; Score 164.6; DB 2; Length 261;
Best Local Similarity 86.7%; Pred. No. 4.4e-29;
Matches 176; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

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Qy      3237 CTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTTCAGTGTAACGGCCTACATTGC 3296
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Qy      3297 CTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTAT 3356
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Db      61 CTTNGCCCTGCNCTCTGTGACCATCAGCTNTAGGCTATACAAGGGTGTGATCCAAGCTAT 120

Qy      3357 CCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATC 3416
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      121 CCAGAAATCAGATGAAGGNCACCCATTCAGGGCATATCTGGANTCTGAAGTTGCTATATC 180

Qy      3417 AGAGGAATTGGTTCAGAAATACA 3439
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Db 181 TGAGGAGTTGNTTCAGAAGTACA 203

RESULT 11

US-08-232-463-14/c

; Sequence 14, Application US/08232463

; Patent No. 5670367

; GENERAL INFORMATION:

; APPLICANT: DORNER, F.

; APPLICANT: SCHEIFLINGER, F.

; APPLICANT: FALKNER, F. G.

; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 1800 Diagonal Road, Suite 500

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22313-0299

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/232,463

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/935,313

; FILING DATE:

; APPLICATION NUMBER: EP 91 114 300.6

; FILING DATE: 26-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 30472/114 IMMU

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)836-9300

; TELEFAX: (703)683-4109

; TELEX: 899149

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7218 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; CLONE: pTZgpt-Fls

US-08-232-463-14

Query Match 2.0%; Score 75.4; DB 1; Length 7218;

Best Local Similarity 5.3%; Pred. No. 1.9e-07;

Matches 22; Conservative 242; Mismatches 153; Indels 0; Gaps 0;

Qy 1127 TTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAA 1186



	Matches	155;	Conservative	0;	Mismatches	133;	Indels	0;	Gaps	0;
Qy	463		CCGCCCCGCCCGCCGCGCCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCC	522						
Db	21936		CCCCGCCCCCCCCGCGCCGCCCCCGCGGGCCCCCAACCCCCCCCCCCCCCCCCCGCGCCC	21995						
Qy	523		CGCGGGCCGCTGCCGGCCGCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGC	582						
Db	21996		CGCCCCCCCCCGCGCCCCCAACCCCCCGCCCCCCCCCCCCCCCCCCCCACC	22055						
Qy	583		AGCCCCGCGGCGCCCGCGCCATCCCTGCCGCGCCGCTGCCGCAGTCCTGCCCTCCAAGCTC	642						
Db	22056		CCCCACACCCGGCCACACGCACCCCCACCCGACGCCCCCGCCCCCCCCCCCCCGCAG	22115						
Qy	643		CCAGAGGACGACGAGCCTCCGGCGAGGCCCCCGCCTCCGCGCCAGCCGGCGGAGCCCC	702						
Db	22116		CCGACGCCCCCCCCCGCGCGCCCCGCCCCGCACCCCGACCCCCCGCGCCCCCGCCC	22175						
Qy	703		CTGGCGGAGCCCGCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC	750						
Db	22176		CCGCCCCCCCCCCCCGCCCCCCCCCGCGGGCGCGGCGCCCCACCCC	22223						

Qy 447 GTCCGCAGCTGCGGTGCCGCCCGCCGCCGCCGCCGCTGCTGGACTTCAGCAGCGACTC 506  
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 Db 1800 GGCGGAGGAGGAGGAGGCGGAGGAGGAGGAGGCGGCGGCGACCGCGGCCTGGGACGACGG 1741  
 Qy 507 GGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCCCCTGCCGCTCCTGAGAGGCA 566  
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 Db 1740 AGACGCCGACGGGGGCGCGGCCGCCCGCGGACGCCGGGGCGAGCGGCCCGTGGCCGCGGTC 1681  
 Qy 567 GCCATCCTGGGAACGCAGCCCCGCGGGCGCCCGCGCCATCCCTGCCGCCCGCTGCCGCAGT 626  
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 Db 1680 GCCCCAGTCCGAGTCCGGGGCCCGCGCGGCGCCGCCCTCTTGGCCCCACCCCCCTGGGG 1621  
 Qy 627 CCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCTCCGGCGAGGCCCCCGCCTCCGCCGCC 686  
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 Db 1620 GGCGAGGGGCGAGCGCGGGGCGGCGGAGGAAGAGGCGGAGGACGAGGCCGCGGGGCCCCGA 1561  
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 Db 1560 GTCCGACCCGCGCCTCTTCCGGGGCGGGCCGCCGCCCTTCCGCGGCGTGGGGGGC 1504

RESULT 14

US-09-103-840A-2/c

; Sequence 2, Application US/09103840A

; Patent No. 6294328

; GENERAL INFORMATION:

; APPLICANT: FLEISCHMAN, Robert D.

; APPLICANT: WHITE, Owen R.

; APPLICANT: FRASER, Claire M.

; APPLICANT: VENTER, John C.

; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

; TITLE OF INVENTION: TUBERCULOSIS

; FILE REFERENCE: 24366-20007.00

; CURRENT APPLICATION NUMBER: US/09/103,840A

; CURRENT FILING DATE: 1998-06-24

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 4403765

; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis

; FEATURE:

; OTHER INFORMATION: CDC 1551

; OTHER INFORMATION: "n" bases at various positions throughout the sequence

; OTHER INFORMATION: represent a, t, c or g

US-09-103-840A-2

Query Match 2.0%; Score 73.2; DB 3; Length 4403765;

Best Local Similarity 52.3%; Pred. No. 2.2e-05;

Matches 162; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

Qy 434 CCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCGCCGCCGCTGCTGGACT 493

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3926287

Qy 494 TCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCCCCTGCCG 553  
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 Db 3926286 CCTTGCCCGCGGCGCCGACAACCCCGCCGGTTCTCCGGTGCCGGCGGCCCCGCGGCC  
 3926227

Qy 554 CTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCGCCATCCCTGCCGC 613  
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 Db 3926226 CGCCGGCGCCGGCGTTACCGCCAGTCCCACCCGCGCCGCGCTCGGCGCCAATCCCGCTGG  
 3926167

Qy 614 CCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCTCCGGCGAGGCCCC 673  
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 Db 3926166 CATTATCAGCACC GGAGCCACCCATGCCGCCGGCGCCGCTTGCCGCCCGGTGCCGCCG  
 3926107

Qy 674 CGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCGCCCCCTTCCACGC 733  
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 Db 3926106 CACCACGGAGCCGTTGATGCCGCCGGCAATGGCGTTGCCGCCCTTGCCGCCGACGCCG  
 3926047

Qy 734 CGGCCGCGCC 743  
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 Db 3926046 CGGCCCGGCC 3926037

RESULT 15

US-09-103-840A-1/c

; Sequence 1, Application US/09103840A

; Patent No. 6294328

; GENERAL INFORMATION:

; APPLICANT: FLEISCHMAN, Robert D.

; APPLICANT: WHITE, Owen R.

; APPLICANT: FRASER, Claire M.

; APPLICANT: VENTER, John C.

; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

; TITLE OF INVENTION: TUBERCULOSIS

; FILE REFERENCE: 24366-20007.00

; CURRENT APPLICATION NUMBER: US/09/103,840A

; CURRENT FILING DATE: 1998-06-24

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 4411529

; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis

; OTHER INFORMATION: H37Rv

US-09-103-840A-1

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 Best Local Similarity 52.3%; Pred. No. 2.2e-05;  
 Matches 162; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

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 Db 3932558 CCGTGCCGGCGCTGCCCGCGCCCGCGCGCCGCTTGCCCGCCGGTGCCGCCGATAACCGG  
 3932499

Qy 494 TCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCCCCTGCCG 553  
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 Db 3932498 CCTTGCCCGCGGCGCCGACAACCCCGCCGGTTCTCCGGTGCCGGCGGCCCCGCGGCC  
 3932439  
  
 Qy 554 CTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCGCCATCCCTGCCGC 613  
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 Db 3932438 CGCCGGCGCCGGCGTTACCGCCAGTCCCACCCGCGCCGCGGTCCGGCGCCAATCCCGCTGG  
 3932379  
  
 Qy 614 CCGCTGCCGAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCTCCGGCGAGGCCCC 673  
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 Db 3932378 CATTATCAGCACCGGAGCCACCCATGCCGCCGGCGCCGCCTTGCGCCGCCGGTGCCGCCGG  
 3932319  
  
 Qy 674 CGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCGCCCCCTTCCACGC 733  
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 Db 3932318 CACCACCGGAGCCGTTGATGCCGCCGGCAATGGCGTTGCCGCCCTGGCCGCCGACGCCGC  
 3932259  
  
 Qy 734 CGGCCGCGCC 743  
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 Db 3932258 CGGCCCCGCC 3932249

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 Job time : 242.145 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 01:22:50 ; Search time 1590.94 Seconds  
(without alignments)  
11831.342 Million cell updates/sec

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Perfect score: 3741  
Sequence: 1 attgctcgtctggtcgccgg.....gattgaagcgcaaagcagat 3741

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
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- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq2:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
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- 18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result                      %  
Query

No.	Score	Match	Length	DB	ID	Description
1	3739.4	100.0	4684	9	US-09-893-348-17	Sequence 17, Appl
2	3065.4	81.9	3492	12	US-10-267-502-214	Sequence 214, App
3	2343.6	62.6	4053	9	US-09-758-140-5	Sequence 5, Appli
4	2343.6	62.6	4053	9	US-09-972-599A-5	Sequence 5, Appli
5	2343.6	62.6	4053	17	US-10-717-597-310	Sequence 310, App
6	2343.6	62.6	4632	15	US-10-060-036-53	Sequence 53, Appl
7	2289.2	61.2	3579	9	US-09-789-386-1	Sequence 1, Appli
8	2289.2	61.2	3579	9	US-09-893-348-22	Sequence 22, Appl
9	2289.2	61.2	3579	12	US-10-267-502-212	Sequence 212, App
10	2289.2	61.2	3579	17	US-10-327-213-8	Sequence 8, Appli
11	2289.2	61.2	3579	17	US-10-466-258-8	Sequence 8, Appli
12	1088.8	29.1	1980	16	US-10-220-891-22	Sequence 22, Appl
13	809.8	21.6	2782	15	US-10-205-194-165	Sequence 165, App
14	497.4	13.3	799	13	US-10-660-946-2	Sequence 2, Appli
15	497.4	13.3	1122	9	US-09-789-386-5	Sequence 5, Appli
16	497.4	13.3	1160	15	US-10-175-523-156	Sequence 156, App
17	497.4	13.3	1785	16	US-10-439-388-62	Sequence 62, Appl
18	497.4	13.3	2052	17	US-10-466-258-3	Sequence 3, Appli
19	497.4	13.3	2235	15	US-10-060-036-54	Sequence 54, Appl
20	495.8	13.3	994	12	US-09-978-360A-110	Sequence 110, App
21	495.8	13.3	1610	9	US-09-765-205-5	Sequence 5, Appli
22	484.8	13.0	2610	17	US-10-641-643-382	Sequence 382, App
23	483.6	12.9	868	9	US-09-789-386-3	Sequence 3, Appli
24	475	12.7	1798	17	US-10-466-258-10	Sequence 10, Appl
25	468	12.5	1514	13	US-09-823-245A-349	Sequence 349, App
26	375.6	10.0	422	9	US-09-960-352-8477	Sequence 8477, Ap
27	374	10.0	422	9	US-09-960-352-11567	Sequence 11567, A
28	322.4	8.6	389	9	US-09-960-352-5154	Sequence 5154, Ap
29	302.6	8.1	423	9	US-09-960-352-9092	Sequence 9092, Ap
30	266.4	7.1	668	16	US-10-264-237-163	Sequence 163, App
31	259	6.9	566	13	US-10-085-783A-17576	Sequence 17576, A
32	259	6.9	566	16	US-10-242-535A-17576	Sequence 17576, A
33	254	6.8	1520	15	US-10-084-817-333	Sequence 333, App
34	253.2	6.8	2331	12	US-10-267-502-213	Sequence 213, App
35	253.2	6.8	3202	9	US-09-954-456-210	Sequence 210, App
36	253.2	6.8	3202	13	US-10-342-887-386	Sequence 386, App
37	253.2	6.8	3202	13	US-10-172-118-386	Sequence 386, App
38	249.2	6.7	431	9	US-09-960-352-2205	Sequence 2205, Ap
39	247.2	6.6	2343	12	US-10-267-502-215	Sequence 215, App
40	244.4	6.5	1502	15	US-10-205-219-94	Sequence 94, Appl
41	242.4	6.5	1473	15	US-10-205-194-128	Sequence 128, App
42	231.8	6.2	3637	16	US-10-108-260A-449	Sequence 449, App
43	231.8	6.2	3637	16	US-10-159-563-443	Sequence 443, App
44	228.8	6.1	711	13	US-10-408-967-1	Sequence 1, Appli
45	228.8	6.1	1330	15	US-10-106-698-1945	Sequence 1945, Ap

#### ALIGNMENTS

##### RESULT 1

US-09-893-348-17

; Sequence 17, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:



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; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 4684
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (253)..(3744)
; OTHER INFORMATION:
US-09-893-348-17

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Query Match          100.0%; Score 3739.4; DB 9; Length 4684;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3740; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 ATTGCTCGTCTGGGCGGCGGGCGGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCG 60
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Db      1 ATTGCTCGTCTGGGCGGCGGGCGGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCG 60

Qy     61 ATCGCGAAGGCAGCAGAAAGCAGTCTCATTGTTCGGGAGCCGTCGCCTCTGCAGGTTCTT 120
        |||
Db     61 ATCGCGAAGGCAGGAGAAGCAGTCTCATTGTTCGGGAGCCGTCGCCTCTGCAGGTTCTT 120

Qy    121 CGGCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACA 180
        |||
Db    121 CGGCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACA 180

Qy    181 ACCGCCCCGCGACTCTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGC 240
        |||
Db    181 ACCGCCCCGCGACTCTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGC 240

Qy    241 GACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGC 300
        |||
Db    241 GACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGC 300

Qy    301 CCGCCCCGGCCTCCGCCCCGCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAG 360
        |||
Db    301 CCGCCCCGGCCTCCGCCCCGCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAG 360

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Qy	361	GACGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTG	420
Db	361	GACGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTG	420
Qy	421	CTGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCGCCGCG	480
Db	421	CTGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCGCCGCG	480
Qy	481	CCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCC	540
Db	481	CCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCC	540
Qy	541	GCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCG	600
Db	541	GCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCG	600
Qy	601	CCATCCCTGCCGCCCGCTGCCGCAGTCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCT	660
Db	601	CCATCCCTGCCGCCCGCTGCCGCAGTCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCT	660
Qy	661	CCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCG	720
Db	661	CCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCG	720
Qy	721	CCCCCTTCCACGCCGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTT	780
Db	721	CCCCCTTCCACGCCGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTT	780
Qy	781	TTTGCTCTTCCTGCTGCATCTGAGCCTGTGATACCCTCCTCTGCAGAAAAAATTATGGAT	840
Db	781	TTTGCTCTTCCTGCTGCATCTGAGCCTGTGATACCCTCCTCTGCAGAAAAAATTATGGAT	840
Qy	841	TTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTG	900
Db	841	TTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTG	900
Qy	901	CTTGAAACTGCTGCCTCTCTTCTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAA	960
Db	901	CTTGAAACTGCTGCCTCTCTTCTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAA	960
Qy	961	CATGGATACCTTGGTAACTTATCAGCAGTGTATCCTCAGAAGGAACAATTGAAGAACT	1020
Db	961	CATGGATACCTTGGTAACTTATCAGCAGTGTATCCTCAGAAGGAACAATTGAAGAACT	1020
Qy	1021	TTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGAT	1080
Db	1021	TTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGAT	1080
Qy	1081	TTAGCAGAATTTTCAGAATTAGAATATTAGAAATGGGATCATCTTTTAAAGGCTCCCCA	1140
Db	1081	TTAGCAGAATTTTCAGAATTAGAATATTAGAAATGGGATCATCTTTTAAAGGCTCCCCA	1140
Qy	1141	AAAGGAGAGTCAGCCATATTAGTAGAAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA	1200
Db	1141	AAAGGAGAGTCAGCCATATTAGTAGAAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA	1200

Qy	1201	GACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCTGTGGGT	1260
Db	1201	GACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCTGTGGGT	1260
Qy	1261	AAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATG	1320
Db	1261	AAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATG	1320
Qy	1321	TCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGG	1380
Db	1321	TCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGG	1380
Qy	1381	GAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTGGAA	1440
Db	1381	GAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTGGAA	1440
Qy	1441	AGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGGAAGGAT	1500
Db	1441	AGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGGAAGGAT	1500
Qy	1501	AGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGACAGC	1560
Db	1501	AGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGACAGC	1560
Qy	1561	TCCAGAGCATATATTACCTGTGCTTCCCTTACCTCAGCAACCGAAAGCACCACAGCAAAC	1620
Db	1561	TCCAGAGCATATATTACCTGTGCTTCCCTTACCTCAGCAACCGAAAGCACCACAGCAAAC	1620
Qy	1621	ACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAAATAGAA	1680
Db	1621	ACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAAATAGAA	1680
Qy	1681	GAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAACGTCAAATCCTTTCCTT	1740
Db	1681	GAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAACGTCAAATCCTTTCCTT	1740
Qy	1741	GTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACT	1800
Db	1741	GTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACT	1800
Qy	1801	GAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGCATGT	1860
Db	1801	GAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGCATGT	1860
Qy	1861	GAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTG	1920
Db	1861	GAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTG	1920
Qy	1921	GTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTGCCCATCA	1980
Db	1921	GTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTGCCCATCA	1980
Qy	1981	TTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTGCCTGATATTGTTATGGAAGCACCA	2040
Db	1981	TTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTGCCTGATATTGTTATGGAAGCACCA	2040
Qy	2041	TTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCACTG	2100

Db	2041	TTAAATTCTCTCCTTCCAAGCGCTGGTGCCTTCTGTAGTGCAGCCAGTGTATCCCCACTG	2100
Qy	2101	GAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAAGCTTGAGCCTGAAAACCCCCACCA	2160
Db	2101	GAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAAGCTTGAGCCTGAAAACCCCCACCA	2160
Qy	2161	TATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAAGAG	2220
Db	2161	TATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAAGAG	2220
Qy	2221	CCTGAAAGTTTAAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGT	2280
Db	2221	CCTGAAAGTTTAAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGT	2280
Qy	2281	GATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTCA	2340
Db	2281	GATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTCA	2340
Qy	2341	GAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCTCTCA	2400
Db	2341	GAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCTCTCA	2400
Qy	2401	CCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCCTGAAGTCCCACAAACA	2460
Db	2401	CCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCCTGAAGTCCCACAAACA	2460
Qy	2461	CAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCC	2520
Db	2461	CAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCC	2520
Qy	2521	CAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAAGCCATATTTAGAG	2580
Db	2521	CAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAAGCCATATTTAGAG	2580
Qy	2581	TCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTG	2640
Db	2581	TCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTG	2640
Qy	2641	ACCAAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAAT	2700
Db	2641	ACCAAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAAT	2700
Qy	2701	GATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCA	2760
Db	2701	GATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCA	2760
Qy	2761	TCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTCAGTGCTAAAGATGATTCTCCT	2820
Db	2761	TCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTCAGTGCTAAAGATGATTCTCCT	2820
Qy	2821	AAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATC	2880
Db	2821	AAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATC	2880
Qy	2881	CAAAGCGGGGCAGATTTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAAT	2940

Db	2881	CAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAAT	2940
Qy	2941	ATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTA	3000
Db	2941	ATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTA	3000
Qy	3001	TCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGC	3060
Db	3001	TCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGC	3060
Qy	3061	AGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACA	3120
Db	3061	AGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACA	3120
Qy	3121	GAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACTTCAGTT	3180
Db	3121	GAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACTTCAGTT	3180
Qy	3181	GTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTA	3240
Db	3181	GTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTA	3240
Qy	3241	TTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTGTCAGTGTAAACGGCCTACATTGCCTTG	3300
Db	3241	TTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTGTCAGTGTAAACGGCCTACATTGCCTTG	3300
Qy	3301	GCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAG	3360
Db	3301	GCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAG	3360
Qy	3361	AAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAG	3420
Db	3361	AAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAG	3420
Qy	3421	GAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACATAAAAGAA	3480
Db	3421	GAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACATAAAAGAA	3480
Qy	3481	CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAAGTGTGATG	3540
Db	3481	CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAAGTGTGATG	3540
Qy	3541	TGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTG	3600
Db	3541	TGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTG	3600
Qy	3601	ATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTAT	3660
Db	3601	ATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTAT	3660
Qy	3661	CTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCT	3720
Db	3661	CTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCT	3720
Qy	3721	GGATTGAAGCGCAAAGCAGAT	3741
Db	3721	GGATTGAAGCGCAAAGCAGAT	3741

RESULT 2

US-10-267-502-214

; Sequence 214, Application US/10267502  
 ; Publication No. US20040071700A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kim, Jaeseob  
 ; APPLICANT: Galant, Ron  
 ; TITLE OF INVENTION: Obesity Linked Genes  
 ; FILE REFERENCE: LSD-07416  
 ; CURRENT APPLICATION NUMBER: US/10/267,502  
 ; CURRENT FILING DATE: 2003-01-27  
 ; NUMBER OF SEQ ID NOS: 439  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 214  
 ; LENGTH: 3492  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 US-10-267-502-214

Query Match 81.9%; Score 3065.4; DB 12; Length 3492;  
 Best Local Similarity 93.6%; Pred. No. 0;  
 Matches 3286; Conservative 0; Mismatches 181; Indels 42; Gaps 7;

Qy	253	ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCT	312
Db	1	ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCGCGATAGCCCGCCCCGGCCC	60
Qy	313	CCGCCCCGCTTCAAGTACCAGTTCTGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG	372
Db	61	CCGCCCCGCTTCAAGTACCAGTTCTGTGACGGAGCCCGAGGACGAGGAGGACGAGGAAGAC	120
Qy	373	GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG	432
Db	121	GAGGAG---GAGGAGGAGGACGACGAGGACCTGGAGGAATTGGAGGTGCTGGAGAGGAAG	177
Qy	433	CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCGCCGCCGCCGCCGCCGCTGCTGGAC	492
Db	178	CCCGCAGCCGGGCTGTCCGCAGTTCCGGT---GCCCCCGCCGCCGCCGCCGCCGCCGCTGCTGGAC	234
Qy	493	TTCAGCAGCGACTCGGTGCCCCCGCGCCCCCGGGCCGCTGCCGGCCGCGCCCCCTGCC	552
Db	235	TTCAGCAGCGACTCGGTGCCCCCGCGCCCCCGGGCCGCTGCCGGCCGCGCCCCCACC	294
Qy	553	GCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCGCCATCCCTGCCG	612
Db	295	GCCCCCTGAGAGGCAGCCGTCTTGGGAACGCAGCCCCGCGGCGTCCGCGCCATCCCTGCCG	354
Qy	613	CCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCTCCGGCGAGGCCC	672
Db	355	CCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCGGAGGACGACGAGCCTCCAGCG-----	408
Qy	673	CCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCCGCCCTTCCACG	732
Db	409	CGGCCTCCGGCGCCAGCCGGCGCGAGCCCCCTAGCGGAGCCCGCCGCCGCCCTTCCACG	468

Qy	733	CCGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTTTTGTCTTCCT	792
Db	469	CCGGCCGCGCCCAAGCGCAGGGGCTCGGGCTCAGTGGATGAGACCCTTTTGTCTTCCT	528
Qy	793	GCTGCATCTGAGCCTGTGATACCCTCCTCTGCAGAAAAAATTATGGATTGATGGAGCAG	852
Db	529	GCTGCATCTGAGCCTGTGATACCCTCCTCTGCAGAAAAAATTATGGATTGAAGGAGCAG	588
Qy	853	CCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAACTGCT	912
Db	589	CCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGTTTGAACTGCT	648
Qy	913	GCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTT	972
Db	649	GCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACACGGATACCTT	708
Qy	973	GGTAACTTATCAGCAGTGTCTCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCT	1032
Db	709	GGTAACTTATCAGCAGTGGCATCCACAGAAGGAACATTGAAGAACTTTAAATGAAGCT	768
Qy	1033	TCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTT	1092
Db	769	TCTAGAGAATTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGAGTCAGCAGAGTTT	828
Qy	1093	TCAGAATTAGAATATTAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCA	1152
Db	829	TCAGTATTAGAATACTCAGAAATGGGATCATCTTTCAATGGCTCCCCAAAAGGAGAGTCA	888
Qy	1153	GCCATATTAGTAGAAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAAGACAAAGAGGAT	1212
Db	889	GCCATGTTAGTAGAAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAAGACAAAGAGGAT	948
Qy	1213	TTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCT-----GTG	1257
Db	949	TTAGTTTGTAGTGCAGCCCTTCATAATCCACAAGAGTCACCTGCGACCCTTACTAAAGTG	1008
Qy	1258	GGTAAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAG	1317
Db	1009	GTTAAAGAAGACGGAGTTATGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGAAA	1068
Qy	1318	ATGTCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCA	1377
Db	1069	ATGTCAGTGGTAGCACCTGTGAGGGAAGAGTATGCAGATTTTAAAGCCATTTGAACAAGCA	1128
Qy	1378	TGGGAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTG	1437
Db	1129	TGGGAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATATG	1188
Qy	1438	GAAAGTAAAGTGGACAGAAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGGAAG	1497
Db	1189	GAAAGTAAAGTGGACAAAAAATGCTTTGAAGATAGCCTGGAGCAAAAAAGTCATGGGAAG	1248
Qy	1498	GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC	1557
Db	1249	GATAGTGAAGGCAGAAATGAGAATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC	1308
Qy	1558	AGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACAGCA	1617

Db	1309	GGCTCCAGAGCGTACATCACCTGTGATTCCCTTTACCTCAGCAACCGAGAGTACTGCAGCA	1368
Qy	1618	AACACTTTCCCTTTGTGTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAAATA	1677
Db	1369	AACATTTTCCCTGTGCTAGAAGATCACACTTCAGAAAATAAAACAGATGAAAAAAAAATA	1428
Qy	1678	GAAGAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTC	1737
Db	1429	GAAGAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTC	1488
Qy	1738	CTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTG	1797
Db	1489	CTTGTAGCAATACATGATTCCGAGGCAGATTATGTCACAACAGATAATTTATCAAAGGTG	1548
Qy	1798	ACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGCA	1857
Db	1549	ACTGAGGCAGTAGTGGCAACCATGCCTGAAGGTCTAACGCCAGATTTAGTTCAGGAAGCA	1608
Qy	1858	TGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGAC	1917
Db	1609	TGTGAAAGTGAAGTGAACGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGAC	1668
Qy	1918	TTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTGCCCA	1977
Db	1669	TTGGTCCAGACATCAGAAGCTATACAAGAGTCAATTTACCCACAGCACAGCTTTGCCCA	1728
Qy	1978	TCATTTGAGGAAGCTGAAGCAACTCCGTCAACAGTTTTGCCTGATATTGTTATGGAAGCA	2037
Db	1729	TCATTTGAGGAAGCTGAAGCAACTCCGTCAACAGTTTTGCCTGATATTGTTATGGAAGCT	1788
Qy	2038	CCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCA	2097
Db	1789	CCATTAAATTCTCTCCTTCCAAGCACTGGTGCTTCTGTAGCGCAGCCCAGTGCATCCCCA	1848
Qy	2098	CTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCCA	2157
Db	1849	CTAGAAGTACCGTCTCCAGTTAGTTATGACGGTATAAAGCTTGAGCCTGAAAATCCCCCA	1908
Qy	2158	CCATATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAA	2217
Db	1909	CCATATGAAGAAGCCATGAGTGTAGCACTAAAAACATCGGACGCAAAGGAAGAAATTAAA	1968
Qy	2218	GAGCCTGAAAGTTTTAATGCAGCTGTTTACAGGAAACAGAAGCTCCTTATATATCCATTGCG	2277
Db	1969	GAGCCTGAAAGTTTTAATGCAGCTGCTCAGGAAGCAGAAGCTCCTTATATATCCATTGCA	2028
Qy	2278	TGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTAT	2337
Db	2029	TGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGGGTTCTCTAATTAT	2088
Qy	2338	TCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCC	2397
Db	2089	TCAGAAATAGCAAAATTTGAGAAGTCGGTACCTGATCACTGTGAGCTCGTGGATGATTCC	2148
Qy	2398	TCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTGAAGTCCCACAA	2457



Db	2149	TCACCCGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCCTGAAGTCCCACAA	2208
Qy	2458	ACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTA	2517
Db	2209	ACACAAGAGGAGGCTGTGATGCTAATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTA	2268
Qy	2518	GCCCAGCACAAA---GAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAGCCATAT	2574
Db	2269	ACACAACACAAACATAAGGAGAGACTTAGTGCCTCACCTCAGGAGGTAGGAAAGCCATAT	2328
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Qy	2695	TCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCA	2754
Db	2449	TCCAATGATGACTTACTTTCTTCTAAGGAAGACAAAATGAAAGAAAGTGAAACATTTTCC	2508
Qy	2755	GATTCATCTCCGATTGAGATAATAGATGAATTTCCCACGTTTGTCAGTGCTAAAGATGAT	2814
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Qy	2815	TCTCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCT	2874
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Db	2740	AGTGTATCTAAGGTGCCCTTATTGCTTCAAATGTTTCTGCTTTGGAATCTCAAATAGAA	2799
Qy	3055	ATGGGCAGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAATTCCTTCT	3114
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Qy	3175	TCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTG---TTTGGT	3231
Db	2920	TCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTATTTGGT	2979
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 Db 3400 GATCATTATCTAGGACTTGCAAACAAGAGCGTTAAGGATGCCATGGCCAAAATCCAAGCA 3459  
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 Db 3460 AAAATCCCTGGATTGAAGCGCAAAGCAGA 3488

# RESULT 3

US-09-758-140-5

; Sequence 5, Application US/09758140

; Patent No. US20020012965A1

; GENERAL INFORMATION:

; APPLICANT: Strittmatter, Stephen M.

; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth

; FILE REFERENCE: 44574-5073-US

; CURRENT APPLICATION NUMBER: US/09/758,140

; CURRENT FILING DATE: 2001-01-12

; PRIOR APPLICATION NUMBER: US 60/175,707

; PRIOR FILING DATE: 2000-01-12

; PRIOR APPLICATION NUMBER: US 60/207,366

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 60/236,378

; PRIOR FILING DATE: 2000-09-29

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 4053

; TYPE: DNA

; ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)..(3710)
; OTHER INFORMATION: Human mRNA for No. US20020012965A1 protein (KIAA0886,
GenBank
; OTHER INFORMATION: Accession No. US20020012965A1 AB020693)
US-09-758-140-5
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Query Match          62.6%;  Score 2343.6;  DB 9;  Length 4053;
Best Local Similarity 81.3%;  Pred. No. 0;
Matches 3017;  Conservative 0;  Mismatches 574;  Indels 119;  Gaps 21;
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Qy      134 CACGACTCGGCCTGCCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACAACCGCCCGCGACT 193
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Db      16 CTCGGCTCAGTCGGCCCAGCCCCCTCTCAGTCCTCCCCAACCCCCACAACCGCCCGCGGCT 75

Qy      194 CTGAGGAGAAGCGGC-CCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCC 252
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Db      76 CTGAGACGCGGCCCCGGCGGCGGCGGCGAGCAGCTGCAGCATCATC-TCCACCCTCCAGCC 134

Qy      253 ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCT 312
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Db      135 ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCTCGGACAGCCACCCCGGCCG 191

Qy      313 CCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG 372
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Db      192 CAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 248

Qy      373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG 432
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Db      249 GAGGAGGAAGAGGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG 308

Qy      433 CCCGACCCGGGCTGTCCGACGTGCGGTGC-----CGCCCGCCGCGCCGCGCCGCTG 486
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Db      309 CCCGCCGCGGGCTGTCCGCGGCCCCAGTGCCCCACCGCCCTGCCGCCGCGCGCCCTG 368

Qy      487 CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCCGGGCCGCTGCCGCCGCGGCC 546
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Db      369 ATGGACTTCGGAATGACTTCGTGCCGCCGCGGCCCGGGGACCCCTGCCGCCGCGCTCCC 428

Qy      547 CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC 597
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Db      429 CCCGTCGCCCCGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCTGTCGACCGTGCCC 488

Qy      598 GCGCCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAG 657
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Db      489 GCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG 548

Qy      658 CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGGAGCCCCCTGGCGGAG----- 711
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Db      549 CCTCCGGCCCGGCTCCCCCTCCTCCCCCGGCCAGCGTGAGCCCCAGGCAGAGCCCGTG 608

Qy      712 -----CCCGCCGCGCCCCCTTCCACGCCGCGCGCCCAAGCGC 750
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Db      609 TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCCGCGCGCCCAAGCGC 668

Qy      751 AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTGTCTTCTGCTGCATCTGAGCCT 807
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Db	669	AGGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTGTCTTCTCCTGCTGCATCTGAGCCT	728
Qy	808	GTGATACCCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT	867
Db	729	GTGATACGCTCCTCTGCAGAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT	785
Qy	868	TCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCCTTCT	927
Db	786	TCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCTTCTCTTCCTTCT	845
Qy	928	CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA	987
Db	846	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	905
Qy	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Db	906	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	965
Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Db	966	GAGAAGGCCAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC	1025
Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
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Qy	1225	GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC	1269
Db	1146	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1205
Qy	1270	AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA	1329
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Qy	1330	GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA	1389
Db	1266	GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA	1325
Qy	1390	GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG	1437
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Db	1383	GAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAAAA	1442
Qy	1498	GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCAGTACCCAGAACCTGTGAAGGAC	1557
Db	1443	GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCAGTACGCCAGAGGTATAAAGGAT	1502
Qy	1558	AGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACCACA	1614

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Qy	1615	GCAAACACTTTTCCTTTTGTAGAAAGATCATACTTCAGAAAAATAAAACAGATGAAAAAAAA	1674
Db	1563	ACAAACATTTTTCTTTTGTAGGAGATCCTACTTCAGAAAAATAAGACCGATGAAAAAAAA	1622
Qy	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT	1731
Db	1623	ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAAC	1682
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Db	1683	CCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA	1742
Qy	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG	1851
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Db	1803	GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA	1862
Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Db	1863	ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT	1922
Qy	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCAACAGTTTGCCTGATATTGTTATG	2031
Db	1923	TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG	1982
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA	2091
Db	1983	GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA	2042
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Db	2043	TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	2099
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Qy	2503	GTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
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Qy	2620	TCTAATGACATTCCAACATTGACCAAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTT	2679
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Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA	2739
Db	2640	AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2699
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Db	2820	CACAAAAGTGAAATTGCTAATGCCCCGATGGAGCTGGGTCAATGCCTTGACAGAAATTG	2879
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)..(3710)
; OTHER INFORMATION: Human DNA encoding for No. US20020077295A1o protein
(KIAA0886, GenBank
; OTHER INFORMATION: Accession No. US20020077295A1 AB020693)
US-09-972-599A-5
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Matches 3017;  Conservative 0;  Mismatches 574;  Indels 119;  Gaps 21;
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Qy      194 CTGAGGAGAAGCGGC-CCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCC 252
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Db      76 CTGAGACGCGGCCCCGGCGGCGGCGGCGAGCAGCTGCAGCATCATC-TCCACCCTCCAGCC 134

Qy      253 ATGGAAGACATAGACCAGTTCGTTCGTTCTCCTCGTCCACGGACAGCCCGCCCGGCCCT 312
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      135 ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCTCGGACAGCCACCCCGGCCG 191

Qy      313 CCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG 372
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      192 CAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 248

Qy      373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG 432
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      249 GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG 308

Qy      433 CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCGCCGCCGCCGCCGCTG 486
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      309 CCCGCCGCCGGGCTGTCCGCAGGCCCCAGTGCCCCACCGCCCCCTGCCGCCGGCGCGCCCCCTG 368

Qy      487 CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCCGGGCCGCTGCCGGCCGCGCCC 546
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      369 ATGGACTTCGGAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC 428

Qy      547 CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC 597
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      429 CCCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCTGTCGACCGTGCCC 488

Qy      598 GCGCCATCCCTGCCGCCCGCTGCCGCAGTCTTGCCCTCCAAGCTCCCAGAGGACGACGAG 657
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      489 GCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG 548

Qy      658 CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGGAGCCCCCTGGCGGAG----- 711
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      549 CCTCCGGCCCCGCCTCCCCCTCCTCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG 608

Qy      712 -----CCCCGCCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC 750
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      609 TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCGGCCGCGCCCAAGCGC 668
```



Qy	751	AGGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTGGCTCTTCCTGCTGCATCTGAGCCT	807
Db	669	AGGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTGGCTCTTCCTGCTGCATCTGAGCCT	728
Qy	808	GTGATACCCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT	867
Db	729	GTGATACGCTCCTCTGCAGAAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT	785
Qy	868	TCGTCCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCCTTCT	927
Db	786	TCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCTTCTCTTCCTTCT	845
Qy	928	CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA	987
Db	846	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAACTTGTCAACA	905
Qy	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Db	906	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	965
Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Db	966	GAGAAGGCAAAAACCTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC	1025
Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Db	1026	TCAGAAATGGGATCATCGTTAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	1085
Qy	1168	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT	1224
Db	1086	AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1145
Qy	1225	GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC	1269
Db	1146	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1205
Qy	1270	AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA	1329
Db	1206	GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGAA	1265
Qy	1330	GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAA	1389
Db	1266	GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAA	1325
Qy	1390	GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG	1437
Db	1326	GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG	1382
Qy	1438	GAAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGAAG	1497
Db	1383	GAAAGTAAAGTGGATAAAAAATGTTTGCAGATAGCCTTGAGCAAACTAATCACGAAAA	1442
Qy	1498	GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC	1557
Db	1443	GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT	1502

Qy	1558	AGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACCACA	1614
Db	1503	CGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA	1562
Qy	1615	GCAAACACTTTCCCTTTGTTAGAAAGATCATACTTCAGAAAAATAAACAGATGAAAAAAAA	1674
Db	1563	ACAAACATTTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAAATAAGACCGATGAAAAAAAA	1622
Qy	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT	1731
Db	1623	ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAAC	1682
Qy	1732	CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Db	1683	CCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA	1742
Qy	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG	1851
Db	1743	AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG	1802
Qy	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Db	1803	GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA	1862
Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Db	1863	ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT	1922
Qy	1972	TGCCCATCATTTTGAGGAAGCTGAAGCAACTCCGTCAACAGTTTTGCCTGATATTGTTATG	2031
Db	1923	TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACAGTTTTGCCTGACATTGTTATG	1982
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA	2091
Db	1983	GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA	2042
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Db	2043	TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	2099
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	2100	CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAAGTATCAGGAATAAAGGAA	2159
Qy	2209	GGAATAAAAGAGCCTGAAAGTTTAAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268
Db	2160	GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA	2219
Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTC	2328
Db	2220	TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTC	2279
Qy	2329	TCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Db	2280	TCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2339
Qy	2389	GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTGAA	2448

Db	2340	GAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2399
Qy	2449	GTCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2400	GTTCCACAAAAACAAGATGAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2459
Qy	2503	GTGTCTGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
Db	2460	TTTGAGTCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCTTTGCCACCTGAGGGA	2519
Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
Db	2520	GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCTGTTA	2579
Qy	2620	TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTT	2679
Db	2580	CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAGCTC	2639
Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA	2739
Db	2640	AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2699
Qy	2740	AGTGAAACATTTTCAGATTCACTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC	2799
Db	2700	ACTGAAACGTTTTCAGATTCACTCCAATTGAAATTATAGATGAGTTCCCTACATTGATC	2759
Qy	2800	AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC	2856
Db	2760	AGTTCTAAAAGTGAATTCATTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC	2819
Qy	2857	GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCAATTGCCTTGCTTAGAATTG	2916
Db	2820	CACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCAATTGCCTTGACAGAATTG	2879
Qy	2917	CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA	2970
Db	2880	CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA	2939
Qy	2971	GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC	3030
Db	2940	GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT	2999
Qy	3031	TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA	3090
Db	3000	TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA	3059
Qy	3091	GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA	3150
Db	3060	GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	3119
Qy	3151	TTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG	3210
Db	3120	TTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG	3179
Qy	3211	AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGC	3270



; SEQ ID NO 310  
; LENGTH: 4053  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-717-597-310

Query Match 62.6%; Score 2343.6; DB 17; Length 4053;  
Best Local Similarity 81.3%; Pred. No. 0;  
Matches 3017; Conservative 0; Mismatches 574; Indels 119; Gaps 21;

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Qy      134 CACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACAACCGCCCCGCGACT 193
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      16  CTCGGCTCAGTCGGCCCAGCCCCTCTCAGTCCTCCCAACCCCCACAACCGCCCCGCGGCT 75

Qy      194 CTGAGGAGAAGCGGC-CCTGCGGGGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCC 252
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      76  CTGAGACGCGGCCCCGGCGGGCGGCAGCAGCTGCAGCATCATC-TCCACCTCCAGCC 134

Qy      253 ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCT 312
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      135 ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCTCGGACAGCCACCCCGGCCG 191

Qy      313 CCGCCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGAGGAG 372
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      192 CAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 248

Qy      373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG 432
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      249 GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG 308

Qy      433 CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCGCCGCGCCGCGCCGCTG 486
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      309 CCCGCCGCGGGCTGTCCGCGGCCCCAGTGCCCCACCGCCCCCTGCCGCCGGCGCGCCCCCTG 368

Qy      487 CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCCGGGGCCGCTGCCGGCCGCGCCC 546
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      369 ATGGACTTCGGAATGACTTCGTGCCGCGCGCCCCGGGACCCCTGCCGCGCGCTCCC 428

Qy      547 CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC 597
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      429 CCCGTCGCCCCGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTCGACCGTGCCC 488

Qy      598 GCGCCATCCCTGCCGCCCCGCTGCCGAGTCTGCCCTCCAAGCTCCCAGAGGACGACGAG 657
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      489 GCGCCATCCCCGCTGTCTGCTGCCGAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG 548

Qy      658 CCTCCGGCGAGGCCCCCGCCTCCGCGCCAGCCGGCGCGAGCCCCCTGGCGGAG----- 711
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      549 CCTCCGGCCCCGCCTCCCCCTCCTCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG 608

Qy      712 -----CCCCGCCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC 750
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      609 TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCCGCCGCGCCCAAGCGC 668

Qy      751 AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 807
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      669 AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 728
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Qy	808	GTGATACCCTCCTCTGCAGAAAAAATTATGGATTGATGGAGCAGCCAGGTAACACTGTT	867
Db	729	GTGATACGCTCCTCTGCAGAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT	785
Qy	868	TCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAACTGCTGCCTCTCTTCCTTCT	927
Db	786	TCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAACTGCTGCTTCTCTTCCTTCT	845
Qy	928	CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA	987
Db	846	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	905
Qy	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Db	906	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	965
Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Db	966	GAGAAGGCAAAAACCTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC	1025
Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Db	1026	TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	1085
Qy	1168	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT	1224
Db	1086	AATCCTAGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1145
Qy	1225	GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC	1269
Db	1146	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1205
Qy	1270	AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA	1329
Db	1206	GAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGAA	1265
Qy	1330	GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA	1389
Db	1266	GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA	1325
Qy	1390	GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG	1437
Db	1326	GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG	1382
Qy	1438	GAAAGTAAAGTGGACAGAAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGAAG	1497
Db	1383	GAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACCTAATCACGAAAAA	1442
Qy	1498	GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC	1557
Db	1443	GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT	1502
Qy	1558	AGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACCACA	1614
Db	1503	CGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA	1562

Qy	1615	GCAAACACTTTCCCTTTGTTAGAAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA	1674
Db	1563	ACAAACATTTTTCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAA	1622
Qy	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT	1731
Db	1623	ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAAC	1682
Qy	1732	CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Db	1683	CCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA	1742
Qy	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG	1851
Db	1743	AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG	1802
Qy	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAAGATTGCTTATGAAACAAA	1911
Db	1803	GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAA	1862
Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Db	1863	ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT	1922
Qy	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	2031
Db	1923	TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTACCAGTTTTGCCTGACATTGTTATG	1982
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGTGGTGCTTCTGTAGTGCAGCCAGTGTA	2091
Db	1983	GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCAGCTCA	2042
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAC	2151
Db	2043	TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAACATGAGCCTGAAAC	2099
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	2100	CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA	2159
Qy	2209	GGAATAAAAGAGCCTGAAAGTTTAAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268
Db	2160	GAAATTAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA	2219
Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTT	2328
Db	2220	TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTT	2279
Qy	2329	TCTAATTATTTCAGAAATAGCAAATTCGAGAAGTCGGTGCCGAACACGCTGAGCTAGTG	2388
Db	2280	TCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATCTGAGCTAGTT	2339
Qy	2389	GAGGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCTGAA	2448
Db	2340	GAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2399
Qy	2449	GTCCCAACAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502

Accession	Position	Sequence	Position
Db	2400	GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2459
Qy	2503	GTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
Db	2460	TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA	2519
Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
Db	2520	GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA	2579
Qy	2620	TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTT	2679
Db	2580	CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTC	2639
Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA	2739
Db	2640	AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2699
Qy	2740	AGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC	2799
Db	2700	ACTGAAACGTTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATC	2759
Qy	2800	AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC	2856
Db	2760	AGTTCTAAAACTGATTCATTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC	2819
Qy	2857	GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTTCATTGCCTTGCTTAGAATTG	2916
Db	2820	CACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTTCATTGCCTTGCACAGAATTG	2879
Qy	2917	CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA	2970
Db	2880	CCCCATGACCTTTCTTTGAAGAACATAACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA	2939
Qy	2971	GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC	3030
Db	2940	GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT	2999
Qy	3031	TCTGCTTTTGGAACTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA	3090
Db	3000	TCTGCTTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA	3059
Qy	3091	GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGAGCTGTA	3150
Db	3060	GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	3119
Qy	3151	TTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG	3210
Db	3120	TTTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG	3179
Qy	3211	AAGACTGGAGTGGTGTTTGGTGCCAGCTTATTCTGCTGCTGTCTCTGACAGTGTTTCAGC	3270
Db	3180	AAGACTGGAGTGGTGTTTGGTGCCAGCCTATTCTGCTGCTTTTCATTGACAGTATTTCAGC	3239
Qy	3271	ATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG	3330





Matches 3017; Conservative 0; Mismatches 574; Indels 119; Gaps 21;

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Qy      134 CACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACAACCGCCCGCGACT 193
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      23  CTCGGCTCAGTCGGCCAGCCCCCTCTCAGTCCTCCCAACCCCCACAACCGCCCGCGGCT 82

Qy     194 CTGAGGAGAAGCGGC-CCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCC 252
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      83  CTGAGACGCGGCCCGGCGGCGGCGGCAGCAGCTGCAGCATCATC-TCCACCTCCAGCC 141

Qy     253 ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCT 312
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     142 ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCTCGGACAGCCACCCCGGCCG 198

Qy     313 CCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG 372
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     199 CAGCCCGCGTTCAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 255

Qy     373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG 432
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     256 GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG 315

Qy     433 CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCGCCCGCCGCGCCGCTG 486
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     316 CCCGCGCCGGGCTGTCCGCGGCCCCAGTGCCACCGCCCTGCCGCGGCGCGCCCTG 375

Qy     487 CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGCGCCGCGCCC 546
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     376 ATGGACTTCGGAAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGCGCGCTCCC 435

Qy     547 CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC 597
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     436 CCCGTCGCCCCGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTGCTCGACCGTGCCC 495

Qy     598 GCGCCATCCCTGCCGCCCGCTGCCGCAGTCTGCCCTCCAAGCTCCCAGAGGACGACGAG 657
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     496 GCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG 555

Qy     658 CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGGAGCCCCCTGGCGGAG----- 711
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     556 CCTCCGGCCCGGCCTCCCCCTCCTCCCCCGGCCAGCGTGAGCCCCAGGCAGAGCCCGTG 615

Qy     712 -----CCCCGCCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC 750
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     616 TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCCGGCCGCGCCCAAGCGC 675

Qy     751 AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 807
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     676 AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 735

Qy     808 GTGATACCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT 867
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     736 GTGATACGCTCCTCTGCAGAAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT 792

Qy     868 TCGTCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAAACTGCTGCCTCTCTTCCTTCT 927
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     793 TCGGCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAAACTGCTGCTTCTCTTCCTTCT 852
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Qy	928	CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACCTTATCAGCA	987
Db	853	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	912
Qy	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Db	913	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	972
Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Db	973	GAGAAGGCAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC	1032
Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Db	1033	TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	1092
Qy	1168	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT	1224
Db	1093	AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1152
Qy	1225	GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC	1269
Db	1153	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1212
Qy	1270	AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA	1329
Db	1213	GAAGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTTAAATGAAAAGAGAGTTGCAGTGGAA	1272
Qy	1330	GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA	1389
Db	1273	GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA	1332
Qy	1390	GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG	1437
Db	1333	GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAATCGAGAGCAACTTG	1389
Qy	1438	GAAAGTAAAGTGACAGAAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGAAG	1497
Db	1390	GAAAGTAAAGTGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAAAAA	1449
Qy	1498	GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGAC	1557
Db	1450	GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT	1509
Qy	1558	AGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACCACA	1614
Db	1510	CGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA	1569
Qy	1615	GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAACAGATGAAAAAAA	1674
Db	1570	ACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAA	1629
Qy	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT	1731
Db	1630	ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAAC	1689

Qy	1732	CCTTTTCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTTACAACAGATACCTTTATCA	1791
Db	1690		
		CCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA	1749
Qy	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG	1851
Db	1750		
		AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCTGACTCCAGATTTAGTACAG	1809
Qy	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAA	1911
Db	1810		
		GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAA	1869
Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Db	1870		
		ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT	1929
Qy	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	2031
Db	1930		
		TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG	1989
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA	2091
Db	1990		
		GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA	2049
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Db	2050		
		TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	2106
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	2107		
		CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA	2166
Qy	2209	GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268
Db	2167		
		GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA	2226
Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTT	2328
Db	2227		
		TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTT	2286
Qy	2329	TCTAATTATTTCAGAAATAGCAAAATTTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Db	2287		
		TCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2346
Qy	2389	GAGGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCCTGAA	2448
Db	2347		
		GAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2406
Qy	2449	GTCCCAACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2407		
		GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2466
Qy	2503	GTGTCTGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
Db	2467		
		TTTGAGTCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCTTTGCCACCTGAGGGA	2526
Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA	2619

Db	2527	 GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA	2586
Qy	2620	TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTT	2679
Db	2587	 CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTC	2646
Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA	2739
Db	2647	 AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2706
Qy	2740	AGTGAAACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC	2799
Db	2707	 ACTGAAACGTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTTCCTACATTGATC	2766
Qy	2800	AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC	2856
Db	2767	 AGTTCATAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC	2826
Qy	2857	GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTG	2916
Db	2827	 CACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCATTGCCTTGCCACAGAATTG	2886
Qy	2917	CCCTGTGACCTTTCTTTCAAGAAATATATATCCTAAAGATGAAG-----TACATGTTTCA	2970
Db	2887	 CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA	2946
Qy	2971	GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC	3030
Db	2947	 GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT	3006
Qy	3031	TCTGCTTTGGAACCTCAGACAGAAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA	3090
Db	3007	 TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA	3066
Qy	3091	GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAAGAGGACAGATCCCTGTGCTGTA	3150
Db	3067	 GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	3126
Qy	3151	TTGTCAGCAGAGCTGAGTAAAACCTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG	3210
Db	3127	 TTTTCAGCAGAGCTGAGTAAAACCTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG	3186
Qy	3211	AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTGAGC	3270
Db	3187	 AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCTGCTGCTTTTCATTGACAGTATTGAGC	3246
Qy	3271	ATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG	3330
Db	3247	 ATTGTCAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG	3306
Qy	3331	ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCA	3390
Db	3307	 ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCA	3366
Qy	3391	TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT	3450



Db	58	CAGCCCGCGTTCAAGTACCAGTTTCGTGAGGGAGCCCCGAGGACGAGGAG---GAAGAAGAG	114
Qy	373	GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAAGTGGAGGTGCTGGAGAGGAAG	432
Db	115	GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG	174
Qy	433	CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCGCCGCCGCCGCGCCGCTG	486
Db	175	CCCGCCGCCGGGCTGTCCGCGGCCCCAGTGCCACCGCCCCCTGCCGCCGGCGCGCCCCCTG	234
Qy	487	CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCC	546
Db	235	ATGGACTTCGAAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC	294
Qy	547	CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC	597
Db	295	CCCGTCGCCCCGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTCGACCGTGCCC	354
Qy	598	GCGCCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAG	657
Db	355	GCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG	414
Qy	658	CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG-----	711
Db	415	CCTCCGGCCCCGGCCTCCCCCTCCTCCCCGGCCAGCGTGAGCCCCAGGCAGAGCCCGTG	474
Qy	712	-----CCCCGCCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC	750
Db	475	TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCGGCCGCGCCCAAGCGC	534
Qy	751	AGGGGCTCC---GGCTCAGTGGATGAGACCCCTTTTGTCTTCTCCTGCTGCATCTGAGCCT	807
Db	535	AGGGGCTCCTCGGGCTCAGTGGATGAGACCCCTTTTGTCTTCTCCTGCTGCATCTGAGCCT	594
Qy	808	GTGATACCCTCCTCTGCAGAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT	867
Db	595	GTGATACGCTCCTCTGCAGAAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT	651
Qy	868	TGCTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCCTTCT	927
Db	652	TCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCTTCTCTTCCTTCT	711
Qy	928	CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA	987
Db	712	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAAATTTGTCAACA	771
Qy	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Db	772	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAAGCTTCTAAAGAGGTCTCA	831
Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Db	832	GAGAAGGCAAAAACCTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC	891
Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167

Db 892 TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 951  
 Qy 1168 AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT 1224  
 || ||| ||||| |||| ||| | |||| || ||||| || ||||| ||| |  
 Db 952 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1011  
 Qy 1225 GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC 1269  
 ||||| | || ||||| | |||| || ||||| ||  
 Db 1012 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1071  
 Qy 1270 AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA 1329  
 ||||| ||||| ||| |||| ||||| ||||| | | |||| | |  
 Db 1072 GAAGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGA 1131  
 Qy 1330 GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA 1389  
 || ||| ||||| || ||||| ||||| || ||||| || ||||| |||||  
 Db 1132 GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA 1191  
 Qy 1390 GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG 1437  
 |||| | ||| | ||| || ||||| ||||| || || || || ||  
 Db 1192 GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG 1248  
 Qy 1438 GAAAGTAAAGTGACAGAAAAATGCTTGAAGATAGCCTGGAGCAAAAAAGTCTTGGGAAG 1497  
 ||||| ||||| || ||||| ||||| ||||| || || | ||  
 Db 1249 GAAAGTAAAGTGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAAAAA 1308  
 Qy 1498 GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC 1557  
 ||||| || || |||| ||| ||||| ||||| ||||| || |||||  
 Db 1309 GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT 1368  
 Qy 1558 AGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCT---CAGCAACCGAAAGCACCACA 1614  
 | | ||||| || ||||| ||||| | ||||| || |||| | |  
 Db 1369 CGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA 1428  
 Qy 1615 GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAA 1674  
 ||||| || ||||| ||||| ||||| ||||| || ||||| |||||  
 Db 1429 ACAAACATTTTCCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAAA 1488  
 Qy 1675 ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT 1731  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1489 ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAAC 1548  
 Qy 1732 CCTTTCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA 1791  
 |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1549 CCTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA 1608  
 Qy 1792 AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG 1851  
 ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1609 AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG 1668  
 Qy 1852 GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA 1911  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1669 GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA 1728  
 Qy 1912 GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT 1971  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1729 ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT 1788



Qy	1972	TGCCCCATCATTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	2031
Db	1789	TGCCCCATCATTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	1848
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCAGTGTA	2091
Db	1849	GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCAGCTCA	1908
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Db	1909	TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	1965
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	1966	CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA	2025
Qy	2209	GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAAGAAACAGAAGCTCCTTATATA	2268
Db	2026	GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA	2085
Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTC	2328
Db	2086	TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTCTGCTGAACCAGCTCCGGATTTC	2145
Qy	2329	TCTAATTATTTCAGAAATAGCAAAATTCGAGAAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Db	2146	TCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2205
Qy	2389	GAGGATTCCCTCACCTGAATCTGAACCAAGTTGACTTATTTAGTGATGATTTCGATTCCTGAA	2448
Db	2206	GAAGATTCCCTCACCTGATTCTGAACCAAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2265
Qy	2449	GTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2266	GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2325
Qy	2503	GTGTCTGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
Db	2326	TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA	2385
Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
Db	2386	GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCTGTTA	2445
Qy	2620	TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTT	2679
Db	2446	CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTC	2505
Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA	2739
Db	2506	AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2565
Qy	2740	AGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC	2799
Db	2566	ACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATC	2625

Qy	2800	AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC	2856
Db	2626	AGTTCTAAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC	2685
Qy	2857	GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTGCTGCCTTGCTTAGAATTG	2916
Db	2686	CACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCATTGCCTTGACAGAAATTG	2745
Qy	2917	CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA	2970
Db	2746	CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA	2805
Qy	2971	GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC	3030
Db	2806	GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT	2865
Qy	3031	TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA	3090
Db	2866	TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA	2925
Qy	3091	GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGAGCTGTA	3150
Db	2926	GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	2985
Qy	3151	TTGTGAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG	3210
Db	2986	TTTTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG	3045
Qy	3211	AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTGAGC	3270
Db	3046	AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTTCATTGACAGTATTGAGC	3105
Qy	3271	ATTGTGAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG	3330
Db	3106	ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG	3165
Qy	3331	ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA	3390
Db	3166	ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA	3225
Qy	3391	TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT	3450
Db	3226	TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT	3285
Qy	3451	CTTGGTCATGTGAACAGCACATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA	3510
Db	3286	CTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA	3345
Qy	3511	GTTGATTCCCTGAAGTTTGAGTGTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT	3570
Db	3346	GTTGATTCTCTGAAGTTTGAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT	3405
Qy	3571	AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT	3630
Db	3406	AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTTCTGTTATTTAT	3465
Qy	3631	GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT	3690



Db	115	GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG	174
Qy	433	CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCCGCCGCCGCCGCCGCTG	486
Db	175	CCCGCCGCCGGGCTGTCCGCGGCCCCAGTGCCACCGCCCCCTGCCGCCGGCGCGCCCTG	234
Qy	487	CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCC	546
Db	235	ATGGACTTCGGAAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC	294
Qy	547	CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC	597
Db	295	CCCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTGACCGTGCCC	354
Qy	598	GCGCCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAG	657
Db	355	GCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG	414
Qy	658	CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG-----	711
Db	415	CCTCCGGCCCCGGCCTCCCCCTCCTCCCCGGCCAGCGTGAGCCCCAGGCAGAGCCCGTG	474
Qy	712	-----CCCCGCCGCCCCCTTCCACGCCGGCCGCGCCCCAAGCGC	750
Db	475	TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCGGCCGCGCCCCAAGCGC	534
Qy	751	AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTTGCTCTCCTGCTGCATCTGAGCCT	807
Db	535	AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTCCTGCTGCATCTGAGCCT	594
Qy	808	GTGATACCCCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT	867
Db	595	GTGATACGCTCCTCTGCAGAAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT	651
Qy	868	TCGTCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAAACTGCTGCCTCTCTTCCTTCT	927
Db	652	TCGGCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAAACTGCTGCTTCTCTTCCTTCT	711
Qy	928	CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA	987
Db	712	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	771
Qy	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Db	772	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	831
Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Db	832	GAGAAGGCAAAAACCTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC	891
Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Db	892	TCAGAAATGGGATCATCGTTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	951
Qy	1168	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT	1224
Db	952	AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1011

Qy 1225 GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC 1269  
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 Db 1012 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1071

Qy 1270 AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA 1329  
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 Db 1072 GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGAA 1131

Qy 1330 GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA 1389  
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 Db 1132 GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA 1191

Qy 1390 GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG 1437  
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 Db 1192 GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG 1248

Qy 1438 GAAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAGTCTTGGGAAG 1497  
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 Db 1249 GAAAGTAAAGTGGATAAAAAATGTTTGCAGATAGCCTTGAGCAAACTAATCACGAAAAA 1308

Qy 1498 GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC 1557  
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 Db 1309 GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT 1368

Qy 1558 AGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCT---CAGCAACCGAAAGCACCACA 1614  
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 Db 1369 CGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA 1428

Qy 1615 GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAAA 1674  
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 Db 1429 ACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAAAA 1488

Qy 1675 ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT 1731  
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 Db 1489 ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAAC 1548

Qy 1732 CCTTTCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA 1791  
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 Db 1549 CCTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA 1608

Qy 1792 AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG 1851  
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 Db 1609 AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG 1668

Qy 1852 GAAGCATGTGAAAGTGAACTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA 1911  
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 Db 1669 GAAGCATGTGAAAGTGAACTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA 1728

Qy 1912 GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT 1971  
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 Db 1729 ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT 1788

Qy 1972 TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG 2031  
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 Db 1789 TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG 1848

Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGT	2091
Db	1849	GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA	1908
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Db	1909	TCACCATTAGAAG--CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	1965
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	1966	CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA	2025
Qy	2209	GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268
Db	2026	GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA	2085
Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC	2328
Db	2086	TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTTC	2145
Qy	2329	TCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Db	2146	TCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTTCTGAGCTAGTT	2205
Qy	2389	GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTGAA	2448
Db	2206	GAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2265
Qy	2449	GTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2266	GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2325
Qy	2503	GTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
Db	2326	TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA	2385
Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
Db	2386	GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA	2445
Qy	2620	TCTAATGACATTCCAACATTGACCAAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTT	2679
Db	2446	CCTGATGAAGTTTCAACATTGAGCAAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTC	2505
Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA	2739
Db	2506	AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2565
Qy	2740	AGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC	2799
Db	2566	ACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATC	2625
Qy	2800	AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC	2856
Db	2626	AGTTCTAAAACCTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC	2685
Qy	2857	GACAAAAGTGAAATTGCTAATATCCAAGCGGGGCAGATTTCATTGCCTTGCTTAGAATTG	2916

Accession	Position	Sequence	Position
Db	2686	CACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCATTGCCTTGCACAGAATTG	2745
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Db	2746	CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA	2805
Qy	2971	GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC	3030
Db	2806	GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT	2865
Qy	3031	TCTGCTTTTGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA	3090
Db	2866	TCTGCTTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA	2925
Qy	3091	GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAAGAGGACAGATCCCTGTGAGCTGTA	3150
Db	2926	GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	2985
Qy	3151	TTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG	3210
Db	2986	TTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG	3045
Qy	3211	AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCTGCTGCTGTCTCTGACAGTGTTTCAGC	3270
Db	3046	AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCTGCTGCTTTTCATTGACAGTATTTCAGC	3105
Qy	3271	ATTGTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG	3330
Db	3106	ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG	3165
Qy	3331	ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA	3390
Db	3166	ATATACAAGGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA	3225
Qy	3391	TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTTCAGAAATACAGTAATTCTGCT	3450
Db	3226	TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGTAATTCTGCT	3285
Qy	3451	CTTGGTCATGTGAACAGCACAAATAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA	3510
Db	3286	CTTGGTCATGTGAAGTGCACGATAAAGGAAGTTCAGGCGCCTCTTCTTAGTTGATGATTTA	3345
Qy	3511	GTTGATTCCCTGAAGTTTGCAGTGTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTTC	3570
Db	3346	GTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT	3405
Qy	3571	AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT	3630
Db	3406	AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACCTCTTCAGTGTTCCTGTTATTTAT	3465
Qy	3631	GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTAAAGGAT	3690
Db	3466	GAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT	3525
Qy	3691	GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA	3740

Db 3526 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3575

RESULT 9

US-10-267-502-212  
; Sequence 212, Application US/10267502  
; Publication No. US20040071700A1  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Jaeseob  
; APPLICANT: Galant, Ron  
; TITLE OF INVENTION: Obesity Linked Genes  
; FILE REFERENCE: LSD-07416  
; CURRENT APPLICATION NUMBER: US/10/267,502  
; CURRENT FILING DATE: 2003-01-27  
; NUMBER OF SEQ ID NOS: 439  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 212  
; LENGTH: 3579  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-267-502-212

Query Match 61.2%; Score 2289.2; DB 12; Length 3579;  
Best Local Similarity 81.5%; Pred. No. 0;  
Matches 2925; Conservative 0; Mismatches 548; Indels 117; Gaps 19;

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Qy      253 ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCGGCCCT 312
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Db      1  ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCTCGGACAGCCACCCCGGCCG 57

Qy      313 CCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG 372
          | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      58 CAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 114

Qy      373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG 432
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Db      115 GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG 174

Qy      433 CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCGCCCGCCCGCGCCGCTG 486
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Db      175 CCCGCCCGGGGCTGTCCGCGGCCCCAGTGCCCAACCGCCCTGCCGCGGCGCGCCCTG 234

Qy      487 CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCC 546
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Db      235 ATGGACTTCGGAATGACTTCGTGCCGCGGCGCCCCGCGGGACCCCTGCCGGCCGCTCCC 294

Qy      547 CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC 597
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Db      295 CCCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTGACCGTGCCC 354

Qy      598 GCGCCATCCCTGCCGCCCCTGCCGCGAGTCTGCCCTCCAAGCTCCCAGAGGACGACGAG 657
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Db      355 GCGCCATCCCCGCTGTCTGCTGCCGCGAGTCTGCCCTCCAAGCTCCCTGAGGACGACGAG 414

Qy      658 CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG----- 711
          ||||| |||| || |||| || || || || || || || || || || || ||
Db      415 CCTCCGGCCCGCCTCCCCCTCCTCCCCGGCCAGCGTGAGCCCCCAGGACAGCCCGTG 474
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Qy 712 -----CCCGCCGCGCCCCCTTCCACGCCGCGCCGCGCCCAAGCGC 750  
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 Db 475 TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTTCCACCCCGCGCCGCGCCCAAGCGC 534

Qy 751 AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 807  
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 Db 535 AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 594

Qy 808 GTGATACCCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT 867  
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 Db 595 GTGATACGCTCCTCTGCAGAAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT 651

Qy 868 TCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAACTGCTGCCTCTCTTCCTTCT 927  
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 Db 652 TCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAACTGCTGCTTCTCTTCCTTCT 711

Qy 928 CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA 987  
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 Db 712 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 771

Qy 988 GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA 1047  
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 Db 772 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 831

Qy 1048 GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT 1107  
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 Db 832 GAGAAGGCAAAAACCTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC 891

Qy 1108 TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA 1167  
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 Db 892 TCAGAAATGGGATCATCGTTTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 951

Qy 1168 AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT 1224  
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Qy 1270 AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA 1329  
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Qy 1390 GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG 1437  
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 Db 1192 GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG 1248

Qy 1438 GAAAGTAAAGTGGACAGAAAATGCTTGAAGATAGCCTGGAGCAAAAAGTCTTGGGAAG 1497  
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 Db 1249 GAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACTAATCACGAAAAA 1308

Qy 1498 GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC 1557  
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Qy 1558 AGCTCCAGAGCATATATTACCTGTGCTTCTTTTACCT---CAGCAACCGAAAGCACCACA 1614  
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 Db 1369 CGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA 1428

Qy 1615 GCAAACACTTTCCCTTTGTTAGAAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA 1674  
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 Db 1429 ACAAACATTTTCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAA 1488

Qy 1675 ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT 1731  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1489 ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAAC 1548

Qy 1732 CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA 1791  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1549 CCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA 1608

Qy 1792 AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTTACAG 1851  
 ||||| ||||| || || || ||||| ||||| ||||| ||||| |||||  
 Db 1609 AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG 1668

Qy 1852 GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA 1911  
 ||||| ||||| ||||| || || ||||| ||||| ||||| ||||| |||||  
 Db 1669 GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA 1728

Qy 1912 GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT 1971  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1729 ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT 1788

Qy 1972 TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG 2031  
 ||||| ||||| || || ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1789 TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG 1848

Qy 2032 GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCAGTGTA 2091  
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 Db 1849 GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCAGCTCA 1908

Qy 2092 TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC 2151  
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 Db 1909 TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC 1965

Qy 2152 CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA 2208  
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 Db 1966 CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA 2025

Qy 2209 GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA 2268  
 | ||| ||||| ||||| | ||||| ||||| ||||| ||||| |||||  
 Db 2026 GAAATTAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA 2085

Qy 2269 TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTT 2328  
 || ||||| ||||| ||||| ||||| ||||| || ||||| |||||  
 Db 2086 TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACAGCTCCGGATTTT 2145

Qy 2329 TCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG 2388

Db	2146	TCTGATTATTTCAGAAATGGCAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2205
Qy	2389	GAGGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCCTGAA	2448
Db	2206	GAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2265
Qy	2449	GTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2266	GTTCCACAAAAACAAGATGAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2325
Qy	2503	GTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
Db	2326	TTTGAGTCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCCTTGCCACCTGAGGGA	2385
Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
Db	2386	GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA	2445
Qy	2620	TCTAATGACATTCCAACATTGACC AAAAGGAGAAAATTTCTTGC AAATGGAAGAGTTT	2679
Db	2446	CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTGCAGATGGAGGAGCTC	2505
Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA	2739
Db	2506	AGTACTGCAGTTTATTCAAATGATGACTTATTATTCTAAGGAAGCACAGATAAGAGAA	2565
Qy	2740	AGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC	2799
Db	2566	ACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATC	2625
Qy	2800	AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC	2856
Db	2626	AGTTCTAAAACTGATTCATTTTCTAAATTAGCCAGGAATATACTGACCTAGAAGTATCC	2685
Qy	2857	GACAAAAGTGAAATTGCTAATATCCAAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTG	2916
Db	2686	CACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCAATTGCCTTGACAGAATTG	2745
Qy	2917	CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA	2970
Db	2746	CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA	2805
Qy	2971	GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC	3030
Db	2806	GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT	2865
Qy	3031	TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA	3090
Db	2866	TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA	2925
Qy	3091	GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGCTGTA	3150
Db	2926	GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	2985
Qy	3151	TTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG	3210

Db 2986 TTTTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG 3045  
 Qy 3211 AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGC 3270  
 |||||  
 Db 3046 AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTTCATTGACAGTATTCAGC 3105  
 Qy 3271 ATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG 3330  
 |||||  
 Db 3106 ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG 3165  
 Qy 3331 ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA 3390  
 |||||  
 Db 3166 ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA 3225  
 Qy 3391 TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT 3450  
 |||||  
 Db 3226 TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT 3285  
 Qy 3451 CTTGGTCATGTGAACAGCACAAATAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA 3510  
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 Db 3286 CTTGGTCATGTGAACAGCACAAATAAAGAACTGAGGCGCCTCTTCTTAGTTGATGATTTA 3345  
 Qy 3511 GTTGATTCCCTGAAGTTTGCAAGTGTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT 3570  
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 Db 3346 GTTGATTCTCTGAAGTTTGCAAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT 3405  
 Qy 3571 AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT 3630  
 |||||  
 Db 3406 AATGGTCTGACACTACTGATTTTGCTCTCATTTCACTCTTCAGTGTTTCTGTTATTTAT 3465  
 Qy 3631 GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT 3690  
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 Db 3466 GAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT 3525  
 Qy 3691 GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740  
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 Db 3526 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3575

RESULT 10

US-10-327-213-8

; Sequence 8, Application US/10327213

; Publication No. US20040121341A1

; GENERAL INFORMATION:

; APPLICANT: FILBIN, MARIE T.

; APPLICANT: DOMENICONI, MARCO

; APPLICANT: CAO, ZIXUAN

; TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)

; TITLE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION

; FILE REFERENCE: CUNY/003

; CURRENT APPLICATION NUMBER: US/10/327,213

; CURRENT FILING DATE: 2002-12-20

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 8

; LENGTH: 3579

; TYPE: DNA

; ORGANISM: Homo sapiens  
US-10-327-213-8

Query Match 61.2%; Score 2289.2; DB 17; Length 3579;  
Best Local Similarity 81.5%; Pred. No. 0;  
Matches 2925; Conservative 0; Mismatches 548; Indels 117; Gaps 19;

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Qy      253 ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCT 312
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1  ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCCTCGGACAGCCACCCCGGCCG 57

Qy      313 CCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG 372
          | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      58  CAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 114

Qy      373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG 432
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      115 GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG 174

Qy      433 CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCGCCGCCCGCGCCGCTG 486
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      175 CCCGCCCGCGGGCTGTCCGCAGCCCACTGCCACCCCTGCCCGCGCGCGCCCTG 234

Qy      487 CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCCGGGCCGCTGCCGGCCGCGCCC 546
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      235 ATGGACTTCGAAATGACTTCGTGCCGCGCGCCCCGGGGACCCCTGCCGGCCGCTCCC 294

Qy      547 CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC 597
          || | ||| || ||| ||||| || ||||| | ||||| | |||||
Db      295 CCCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCTCGTCCGACCGTGCCC 354

Qy      598 GCGCCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAG 657
          ||||| ||||| || | ||||| ||||| ||||| ||||| ||||| |||||
Db      355 GCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG 414

Qy      658 CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGGAGCCCCCTGGCGGAG----- 711
          ||||| ||||| ||||| ||||| || ||||| || ||||| || |||||
Db      415 CCTCCGGCCCCGGCCTCCCCCTCCTCCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG 474

Qy      712 -----CCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC 750
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      475 TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCGGCCGCGCCCAAGCGC 534

Qy      751 AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTGTCTCTTCTGCTGCATCTGAGCCT 807
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      535 AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTGTCTCTTCTGCTGCATCTGAGCCT 594

Qy      808 GTGATACCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT 867
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      595 GTGATACGCTCCTCTGCAGAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT 651

Qy      868 TCGTCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAACTGCTGCCTCTCTTCCTTCT 927
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      652 TCGGCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAACTGCTGCTTCTCTTCCTTCT 711

Qy      928 CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACCTTATCAGCA 987
          || ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
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Db	712	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	771
Qy	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Db	772	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	831
Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Db	832	GAGAAGGCAAAAACCTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC	891
Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Db	892	TCAGAAATGGGATCATCGTTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	951
Qy	1168	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT	1224
Db	952	AATCCTAGGGAAGAAATAATCGTGAAAAATAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1011
Qy	1225	GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC	1269
Db	1012	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1071
Qy	1270	AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTTAATGAAATGCAGATGTCAGTAGTA	1329
Db	1072	GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTTTAATGAAAAGAGAGTTGTCAGTGGAA	1131
Qy	1330	GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA	1389
Db	1132	GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA	1191
Qy	1390	GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG	1437
Db	1192	GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAAATCGAGAGCAACTTG	1248
Qy	1438	GAAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGAAG	1497
Db	1249	GAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACTAATCACGAAAAA	1308
Qy	1498	GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC	1557
Db	1309	GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT	1368
Qy	1558	AGCTCCAGAGCATATATTACCTGTGCTTCCCTTTACCT---CAGCAACCGAAAGCACCACA	1614
Db	1369	CGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA	1428
Qy	1615	GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA	1674
Db	1429	ACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAA	1488
Qy	1675	ATAGAAGAAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAACGTCAAAT	1731
Db	1489	ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAAC	1548
Qy	1732	CCTTTCCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Db	1549	CCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA	1608

Qy	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTAGTTCAG	1851
Db	1609	AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCTGACTCCAGATTAGTACAG	1668
Qy	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Db	1669	GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA	1728
Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Db	1729	ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT	1788
Qy	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	2031
Db	1789	TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG	1848
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGTCTCTGTAGTGCAGCCCAGTGTA	2091
Db	1849	GAAGCACCATTGAATTCTGCAGTTCCTAGTGTCTGGTGTCTCCGTGATACAGCCCAGCTCA	1908
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Db	1909	TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	1965
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	1966	CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA	2025
Qy	2209	GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268
Db	2026	GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA	2085
Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTT	2328
Db	2086	TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTT	2145
Qy	2329	TCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Db	2146	TCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2205
Qy	2389	GAGGATTCCCTCACCTGAATCTGAACAGTTGACTTATTTAGTGATGATTGATTCCCTGAA	2448
Db	2206	GAAGATTCCCTCACCTGATTCTGAACAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2265
Qy	2449	GTCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2266	GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2325
Qy	2503	GTGTCTGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
Db	2326	TTTGAGTCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCTTTGCCACCTGAGGGA	2385
Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
Db	2386	GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCTGTTA	2445

Qy	2620	TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTT	2679
Db	2446	CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTC	2505
Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA	2739
Db	2506	AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2565
Qy	2740	AGTGAAACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC	2799
Db	2566	ACTGAAACGTTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTCCCTACATTGATC	2625
Qy	2800	AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC	2856
Db	2626	AGTTCATAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC	2685
Qy	2857	GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTG	2916
Db	2686	CACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCATTGCCTTGCCACAGAATTG	2745
Qy	2917	CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA	2970
Db	2746	CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA	2805
Qy	2971	GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC	3030
Db	2806	GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT	2865
Qy	3031	TCTGCTTTGGAACCTCAGACAGAAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA	3090
Db	2866	TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA	2925
Qy	3091	GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA	3150
Db	2926	GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	2985
Qy	3151	TTGTCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG	3210
Db	2986	TTTTCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG	3045
Qy	3211	AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGC	3270
Db	3046	AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTTCCTGCTGCTTTTCATTGACAGTATTTCAGC	3105
Qy	3271	ATTGTGAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG	3330
Db	3106	ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG	3165
Qy	3331	ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA	3390
Db	3166	ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA	3225
Qy	3391	TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTTCAGAAATACAGTAATTCTGCT	3450
Db	3226	TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAAGTACAGTAATTCTGCT	3285
Qy	3451	CTTGGTCATGTGAACAGCACATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA	3510





Qy	433	CCCGCAGCCCGGGCTGTCCCGCAGCTGCGGTGC-----CGCCCCGCCGCCGCCGCCGCCGCTG	486
Db	175	CCCGCCGCCGGGCTGTCCGCGGGCCCCAGTGCCACCGCCCCCTGCCGCCGCCGCCGCCCTG	234
Qy	487	CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCC	546
Db	235	ATGGACTTCGGAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC	294
Qy	547	CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC	597
Db	295	CCCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTGACCGTGCCC	354
Qy	598	GCGCCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCAGAGGACGACGAG	657
Db	355	GCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG	414
Qy	658	CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG-----	711
Db	415	CCTCCGGCCCCGGCCTCCCCCTCCTCCCCGGCCAGCGTGAGCCCCAGGCAGAGCCCGTG	474
Qy	712	-----CCCCGCCGCCGCCCTTCCACGCCGGCCGCGCCCAAGCGC	750
Db	475	TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCCGCCGCGCCCAAGCGC	534
Qy	751	AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT	807
Db	535	AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT	594
Qy	808	GTGATACCCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT	867
Db	595	GTGATACGCTCCTCTGCAGAAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT	651
Qy	868	TCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCCTTCT	927
Db	652	TCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCTTCTCTTCCTTCT	711
Qy	928	CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA	987
Db	712	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	771
Qy	988	GTGTCACTCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Db	772	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	831
Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Db	832	GAGAAGGCAAAAACCTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC	891
Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Db	892	TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	951
Qy	1168	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT	1224
Db	952	AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1011
Qy	1225	GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC	1269

Db	1012	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1071
Qy	1270	AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA	1329
Db	1072	GAAGTTGTGTCTTCAGAAAAGCAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGAA	1131
Qy	1330	GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA	1389
Db	1132	GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA	1191
Qy	1390	GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG	1437
Db	1192	GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG	1248
Qy	1438	GAAAGTAAAGTGGACAGAAAATGCTTGAAGATAGCCTGGAGCAAAAAGTCTTGGGAAG	1497
Db	1249	GAAAGTAAAGTGGATAAAAAATGTTTGCAGATAGCCTTGAGCAAATAATCACGAAAAA	1308
Qy	1498	GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC	1557
Db	1309	GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT	1368
Qy	1558	AGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCT---CAGCAACCGAAAGCACCACA	1614
Db	1369	CGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATTGCA	1428
Qy	1615	GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA	1674
Db	1429	ACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAA	1488
Qy	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT	1731
Db	1489	ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAAC	1548
Qy	1732	CCTTTTCTTGTTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Db	1549	CCTTTTCTTGTTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA	1608
Qy	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG	1851
Db	1609	AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG	1668
Qy	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Db	1669	GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA	1728
Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Db	1729	ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT	1788
Qy	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	2031
Db	1789	TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG	1848
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCAGTGTA	2091

Db	1849	GAAGCACCATTGAATTCTGCAGTTCCTAGTGTGGTGCTTCCGTGATACAGCCCAGCTCA	1908
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAAGCTTGAGCCTGAAAAC	2151
Db	1909	TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	1965
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	1966	CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAAGTATCAGGAATAAAGGAA	2025
Qy	2209	GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268
Db	2026	GAAATTAAAGAGCCTGAAAAATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA	2085
Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC	2328
Db	2086	TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTTC	2145
Qy	2329	TCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Db	2146	TCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2205
Qy	2389	GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTGAA	2448
Db	2206	GAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2265
Qy	2449	GTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2266	GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2325
Qy	2503	GTGTCTGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
Db	2326	TTTGAGTCAATGATAGAATATGAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA	2385
Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
Db	2386	GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCGTGTTA	2445
Qy	2620	TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTT	2679
Db	2446	CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAGCTC	2505
Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA	2739
Db	2506	AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2565
Qy	2740	AGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC	2799
Db	2566	ACTGAAACGTTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCTACATTGATC	2625
Qy	2800	AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC	2856
Db	2626	AGTTCTAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC	2685
Qy	2857	GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTTCATTGCCTTGCTTAGAATTG	2916
Db	2686	CACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTTCATTGCCTTGACACAGAATTG	2745

Qy	2917	CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA	2970
Db	2746	CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA	2805
Qy	2971	GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC	3030
Db	2806	GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT	2865
Qy	3031	TCTGCTTTGGAACTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA	3090
Db	2866	TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA	2925
Qy	3091	GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGAGCTGTA	3150
Db	2926	GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	2985
Qy	3151	TTGTGAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG	3210
Db	2986	TTTTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG	3045
Qy	3211	AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGC	3270
Db	3046	AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGC	3105
Qy	3271	ATTGTCAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG	3330
Db	3106	ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG	3165
Qy	3331	ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCA	3390
Db	3166	ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCA	3225
Qy	3391	TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT	3450
Db	3226	TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGTTTCAGAAAGTACAGTAATTCTGCT	3285
Qy	3451	CTTGGTCATGTGAACAGCACATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA	3510
Db	3286	CTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA	3345
Qy	3511	GTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT	3570
Db	3346	GTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT	3405
Qy	3571	AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT	3630
Db	3406	AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTTCTGTTATTTAT	3465
Qy	3631	GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT	3690
Db	3466	GAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT	3525
Qy	3691	GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA	3740
Db	3526	GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA	3575

RESULT 12  
 US-10-220-891-22  
 ; Sequence 22, Application US/10220891  
 ; Publication No. US20030207286A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NAKAGAWARA, AKIRA  
 ; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES HAVING CHARACTERISTICS OF ENHANCED  
 ; TITLE OF INVENTION: EXPRESSION IN HUMAN NEUROBLASTOMA WITH FAVORABLE  
 PROGNOSIS  
 ; TITLE OF INVENTION: BASED ON COMPARISON BETWEEN HUMAN NEUROBLASTOMA WITH  
 FAVORABLE  
 ; TITLE OF INVENTION: PROGNOSIS AND HUMAN NEUROBLASTOMA WITH UNFAVORABLE  
 PROGNOSIS  
 ; FILE REFERENCE: 7388-73435  
 ; CURRENT APPLICATION NUMBER: US/10/220,891  
 ; CURRENT FILING DATE: 2003-03-07  
 ; PRIOR APPLICATION NUMBER: JP 2000/140387  
 ; PRIOR FILING DATE: 2000-05-12  
 ; PRIOR APPLICATION NUMBER: JP 2000/159195  
 ; PRIOR FILING DATE: 2000-03-07  
 ; NUMBER OF SEQ ID NOS: 108  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 22  
 ; LENGTH: 1980  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-220-891-22

Query Match 29.1%; Score 1088.8; DB 16; Length 1980;  
 Best Local Similarity 83.5%; Pred. No. 3.8e-275;  
 Matches 1289; Conservative 0; Mismatches 237; Indels 18; Gaps 4;

Qy	2215	AAAGAGCCTGAAAGTTTAAATGCAGCTGTTCAAGAAACAGAAGCTCCTTATATATCCATT	2274
Db	28	AAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATATCTATT	87
Qy	2275	GCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAAT	2334
Db	88	GCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTCTCTGAT	147
Qy	2335	TATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGAT	2394
Db	148	TATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTTGAAGAT	207
Qy	2395	TCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCTGAAGTCCCA	2454
Db	208	TCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGACGTTCCA	267
Qy	2455	CAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----AGTGTCT	2508
Db	268	CAAAACAAGGTGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCATTTGAG	327
Qy	2509	GAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCTCACCTCAGGAGCTAGGAAAG	2568
Db	328	TCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGAGGAAAG	387

Qy 2569 CCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCATCTAAT 2625  
 ||||| || ||||| || || ||||| || ||||| || |||||  
 Db 388 CCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTACCTGAT 447

Qy 2626 GACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATACT 2685  
 || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 448 GAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTCAGTACT 507

Qy 2686 GCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAA 2745  
 ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 508 GCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAAACTGAA 567

Qy 2746 ACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTGCTGCT 2805  
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 568 ACGTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTTCCTACATTGATCAGTCCT 627

Qy 2806 AAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAA 2862  
 ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 628 AAAACTGATTCATTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCCACAAA 687

Qy 2863 AGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTGCCCTGT 2922  
 ||||| ||||| || || || || ||||| ||||| ||||| |||||  
 Db 688 AGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCATTGCCTTGACACAGAATTGCCCCAT 747

Qy 2923 GACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCAGATGAA 2976  
 ||||| ||||| ||||| || || ||||| ||||| || || ||||| |||||  
 Db 748 GACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCAGATGAC 807

Qy 2977 TTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCT 3036  
 || || ||||| ||||| || || ||||| || || ||||| || ||||| |||||  
 Db 808 TTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTTTCTGCT 867

Qy 3037 TTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAAGAAGCA 3096  
 ||||| ||||| ||||| || || ||||| ||||| ||||| ||||| |||||  
 Db 868 TTGGCCACTCAGGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTAAGAAGCT 927

Qy 3097 GAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGCTGTATTGTCA 3156  
 ||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||  
 Db 928 GAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATATTTTCA 987

Qy 3157 GCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACT 3216  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 988 GCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACT 1047

Qy 3217 GGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTC 3276  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1048 GGAGTGGTGTGTTGGTGCCAGCCTATTCAGCTGCTTTTCATTGACAGTATTTCAGCATTGTC 1107

Qy 3277 AGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATAT 3336  
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1108 AGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATAC 1167

Qy 3337 AAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATTTA 3396  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1168 AAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTG 1227

Qy 3397 GAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGT 3456

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Db      1228  ||||| GAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGT 1287
Qy      3457  CATGTGAACAGCACAAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGAT 3516
Db      1288  ||||| CATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGAT 1347
Qy      3517  TCCCTGAAGTTTGCAGTGTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGT 3576
Db      1348  ||||| TCTCTGGAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTAATGGT 1407
Qy      3577  CTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGG 3636
Db      1408  ||||| CTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTTCTGTTATTTATGAACGG 1467
Qy      3637  CATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATG 3696
Db      1468  ||||| CATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATG 1527
Qy      3697  GCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
Db      1528  ||||| GCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 1571

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# RESULT 13

US-10-205-194-165

; Sequence 165, Application US/10205194

; Publication No. US20030134301A1

; GENERAL INFORMATION:

; APPLICANT: Warner-Lambert Company

; APPLICANT: Lee, Kevin

; APPLICANT: Dixon, Alistair

; APPLICANT: Brooksbank, Robert

; APPLICANT: Pinnock, Robert

; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain

; FILE REFERENCE: WL-A-018201

; CURRENT APPLICATION NUMBER: US/10/205,194

; CURRENT FILING DATE: 5200-07-24

; PRIOR APPLICATION NUMBER: GB 0118354.0

; PRIOR FILING DATE: 2001-07-27

; NUMBER OF SEQ ID NOS: 177

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 165

; LENGTH: 2782

; TYPE: DNA

; ORGANISM: Rattus norvegicus

; FEATURE:

; OTHER INFORMATION: Foocen-m2 reticulon

US-10-205-194-165

Query Match 21.6%; Score 809.8; DB 15; Length 2782;

Best Local Similarity 99.8%; Pred. No. 1.5e-201;

Matches 811; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 14 GCGGCGGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCGATCGCGAAGGCAG 73

Db 462 GCGGCGGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCGATCGCGAAGGCAG 521



Qy	74	CAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTTCGGCTCGGCTCGG	133
Db	522	GAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTTCGGCTCGGCTCGG	581
Qy	134	CACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCCAACCCCCACAACCGCCCGCGACT	193
Db	582	CACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCCAACCCCCACAACCGCCCGCGACT	641
Qy	194	CTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCCA	253
Db	642	CTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCCA	701
Qy	254	TGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCTC	313
Db	702	TGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCTC	761
Qy	314	CGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAGG	373
Db	762	CGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAGG	821
Qy	374	AGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAGC	433
Db	822	AGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAGC	881
Qy	434	CCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCCGCCGCGCTGCTGGACT	493
Db	882	CCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCCGCCGCGCTGCTGGACT	941
Qy	494	TCAGCAGCGACTCGGTGCCCCCGCGCCCCCGGGCCGCTGCCGGCCGCGCCCCCTGCCG	553
Db	942	TCAGCAGCGACTCGGTGCCCCCGCGCCCCCGGGCCGCTGCCGGCCGCGCCCCCTGCCG	1001
Qy	554	CTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCGCCATCCCTGCCGC	613
Db	1002	CTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCGCCATCCCTGCCGC	1061
Qy	614	CCGCTGCCGAGTCTTGCCCTCCAAGCTCCCAGAGGACGACGAGCCTCCGGCGAGGCCCC	673
Db	1062	CCGCTGCCGAGTCTTGCCCTCCAAGCTCCCAGAGGACGACGAGCCTCCGGCGAGGCCCC	1121
Qy	674	CGCTCCGCCGCCAGCCGGCGGAGCCCCCTGGCGGAGCCCGCCGCGCCCCCTTCCACGC	733
Db	1122	CGCTCCGCCGCCAGCCGGCGGAGCCCCCTGGCGGAGCCCGCCGCGCCCCCTTCCACGC	1181
Qy	734	CGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTG	793
Db	1182	CGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTG	1241
Qy	794	CTGCATCTGAGCCTGTGATACCCTCCTCTGCAG	826
Db	1242	CTGCATCTGAACCTGTGATACCCTCCTCTGCAG	1274

RESULT 14

US-10-660-946-2

; Sequence 2, Application US/10660946

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; Publication No. US20040063131A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Au-Young, Janice
; Goli, Surya K.
; Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/660,946
; FILING DATE: 12-Sep-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/228,213A
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/700,607
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 799 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: <Unknown>
; CLONE: Consensus
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-660-946-2

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Query Match          13.3%; Score 497.4; DB 13; Length 799;
Best Local Similarity 92.7%; Pred. No. 1e-119;
Matches 522; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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Qy      3178 GTTGTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 3237
          |||
Db      108 GTTGTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 167
          |||
Qy      3238 TTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTCAGTGTAACGGCCTACATTGCC 3297

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; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
US-09-789-386-5

Query Match 13.3%; Score 497.4; DB 9; Length 1122;  
Best Local Similarity 92.7%; Pred. No. 1.3e-119;  
Matches 522; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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Qy      3178 GTTGTGGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 3237
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Db      556 GTTGTGGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 615

Qy      3238 TTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTGAGTGTAAACGGCCTACATTGCC 3297
          |||
Db      616 CTATTCCTGCTGCTTTCATTGACAGTATTTCAGCATTGTGAGCGTAAACAGCCTACATTGCC 675

Qy      3298 TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATC 3357
          |||
Db      676 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 735

Qy      3358 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCA 3417
          |||
Db      736 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 795

Qy      3418 GAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAA 3477
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Db      796 GAGGAGTTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAAGTGCACGATAAAG 855

Qy      3478 GAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTG 3537
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Db      856 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 915

Qy      3538 ATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCT 3597
          |||
Db      916 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT 975

Qy      3598 CTGATCTCACTCTTCAGTATTCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCAT 3657
          |||
Db      976 CTCATTTCACTCTTCAGTGTTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1035

Qy      3658 TATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATC 3717
          |||
Db      1036 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 1095

Qy      3718 CCTGGATTGAAGCGCAAAGCAGA 3740
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Db      1096 CCTGGATTGAAGCGCAAAGCTGA 1118
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Search completed: September 11, 2004, 16:03:44  
Job time : 1604.94 secs